```
RESULT 8
Q8UVX5
ID   Q8UVX5      PRELIMINARY;      PRT;   127 AA.
AC   Q8UVX5;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Onconase precursor.
GN   RPR.
OS   Rana pipiens (Northern leopard frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8404;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Liao Y.-D., Wang S.-C.;
RT   "Rana pipiens onconase genomic DNA.";
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF332139; AAL54383.1; -.
DR   PIR; A39035; A39035.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     23       POTENTIAL.
SQ   SEQUENCE   127 AA;  14469 MW;  953F90D351CFEEF3 CRC64;

  Query Match             45.6%;  Score 273.5;  DB 13;  Length 127;
  Best Local Similarity   48.6%;  Pred. No. 1.2e-23;
  Matches   54;  Conservative   16;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          1 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58
              |:| |||:||| ||  : |: |:  |::     ||  |||| |    ||||| |:| : |
Db         24 QDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 79

Qy         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         80 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 127


RESULT 9
Q9DFY6
ID   Q9DFY6      PRELIMINARY;      PRT;   129 AA.
AC   Q9DFY6;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RC-RNase4 ribonuclease precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20512555; PubMed=11058105;
RA   Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT   "Purification and cloning of cytotoxic ribonucleases from Rana
RT   catesbeiana (bullfrog).";
RL   Nucleic Acids Res. 28:4097-4104(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF242555; AAG31441.2; -.
DR   PDB; 1KVZ; 28-JUL-02.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24    129       RC-RNASE4 RIBONUCLEASE.
SQ   SEQUENCE   129 AA;  14724 MW;  826A62882B10ABDA CRC64;

  Query Match             40.5%;  Score 243;  DB 13;  Length 129;
  Best Local Similarity   42.5%;  Pred. No. 4e-20;
  Matches   48;  Conservative   25;  Mismatches   30;  Indels   10;  Gaps    5;

Qy          1 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58
              |:||||::||: :|  : |: ::  :::     ||  |||| |    |||:| ||| : :
Db         24 QDWATFKKKHLTDTWDVDCDNLMPTSLF----DCKDKNTFIYSLPGPVKALCRGVIFSAD 79

Qy         59 VLSTTRFQLNTCTRTSITPR-PCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
              ||| : | |  |   :: || || |  :  :| ||::||:: |||||:| ||
Db         80 VLSNSEFYLAEC---NVKPRKPCKYKLKKSSNRICIRCEHELPVHFAGVGICP 129


RESULT 10
Q9DFY8
ID   Q9DFY8      PRELIMINARY;      PRT;   128 AA.
AC   Q9DFY8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RC-RNase2 ribonuclease precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20512555; PubMed=11058105;
RA   Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT   "Purification and cloning of cytotoxic ribonucleases from Rana
RT   catesbeiana (bullfrog).";
RL   Nucleic Acids Res. 28:4097-4104(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF242553; AAG31439.1; -.
DR   PDB; 1M58; 09-JAN-03.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24    128       RC-RNASE2 RIBONUCLEASE.
SQ   SEQUENCE   128 AA;  14839 MW;  989719CF52053ECC CRC64;

  Query Match             37.6%;  Score 225.5;  DB 13;  Length 128;
  Best Local Similarity   39.3%;  Pred. No. 4.1e-18;
  Matches   44;  Conservative   21;  Mismatches   38;  Indels    9;  Gaps    4;

Qy          1 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58
              ||| |||:||: :|  : |:  :   ::     ||: |||| :    |:|:|  :| : |
Db         24 QNWETFQKKHLTDTRDVKCDAEMKKALF----DCKQKNTFIYARPGRVQALCKNIIVSKN 79

Qy         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
              |||  | |: | |  :   || |  :  :| ||: |||: ||||  :  ||
Db         80 VLSTDEFYLSDCNRIKL---PCHYKLKKSSNTICITCENKLPVHFVAVEECP 128
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RESULT 5
Q98SM1
ID   Q98SM1      PRELIMINARY;      PRT;   132 AA.
AC   Q98SM1;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RNase A-type ribonuclease rc204 precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21539506; PubMed=11683320;
RA   Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT   "Rapid diversification of RNase A superfamily ribonuclease from the
RT   bullfrog, Rana catesbeiana.";
RL   J. Mol. Evol. 53:31-38(2001).
DR   EMBL; AF351208; AAK30254.1; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     22       POTENTIAL.
SQ   SEQUENCE   132 AA;  14704 MW;  95D61760F729868E CRC64;

  Query Match             74.1%;  Score 444.5;  DB 13;  Length 132;
  Best Local Similarity   77.3%;  Pred. No. 2.6e-43;
  Matches   85;  Conservative    8;  Mismatches   16;  Indels    1;  Gaps    1;

Qy          1 QNWATFQQKHIINTPII-CNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 59
              |:| ||||||| :|  | ||||:| :|||| ||||:|||||| ||||||||||||:| ||
Db         23 QDWPTFQQKHIPSTSSIDCNTIMDKDIYIVRGQCKKVNTFIIYSATTVKAICTGVLNSNV 82

Qy         60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              ||||||||   ||| || |||||||  ||| |||||||:|||||||:|
Db         83 LSTTRFQLXXXTRTFITSRPCPYSSTKETNKICVKCENEYPVHFAGIGKC 132


RESULT 6
Q9DF78
ID   Q9DF78      PRELIMINARY;      PRT;   132 AA.
AC   Q9DF78;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RC-RNaseL1 ribonuclease precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20512555; PubMed=11058105;
RA   Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT   "Purification and cloning of cytotoxic ribonucleases from Rana
RT   catesbeiana (bullfrog).";
RL   Nucleic Acids Res. 28:4097-4104(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF288642; AAG30414.2; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    132       RC-RNASEL1 RIBONUCLEASE.
SQ   SEQUENCE   132 AA;  14625 MW;  D8D9A517452FBE53 CRC64;

  Query Match             62.0%;  Score 372;  DB 13;  Length 132;
  Best Local Similarity   64.9%;  Pred. No. 5.8e-35;
  Matches   72;  Conservative   10;  Mismatches   27;  Indels    2;  Gaps    2;

Qy          1 QNWATFQQKHIINTPII-CNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58
              |||| |::||| :|  | ||||:|  ||||||:||  |||||||   |||||:||  :
Db         22 QNWAKFKEKHITSTSSIDCNTIMDKAIYIVGGKCKERNTFIISSEDNVKAICSGVSPDRK 81

Qy         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              |||| |:|||| | |||||||||     : | |||||| | |||| |||:|
Db         82 ELSTTSFKLNTCIRDSITPRPCPYHPSPDNNKICVKCEKQLPVHFVGIGKC 132


RESULT 7
Q9I8V8
ID   Q9I8V8      PRELIMINARY;      PRT;   127 AA.
AC   Q9I8V8;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Onconase variant rapLR1 precursor.
OS   Rana pipiens (Northern leopard frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8404;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20330357; PubMed=10871370;
RA   Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;
RT   "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a
RT   3' UTR of unusual length and structure.";
RL   Nucleic Acids Res. 28:2375-2382(2000).
DR   EMBL; AF165133; AAF76935.1; -.
DR   PIR; A39035; A39035.
DR   HSSP; P22069; 1ONC.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     23       POTENTIAL.
SQ   SEQUENCE   127 AA;  14491 MW;  B8511DC5407AB69B CRC64;

  Query Match             46.2%;  Score 277.5;  DB 13;  Length 127;
  Best Local Similarity   48.6%;  Pred. No. 4.2e-24;
  Matches   54;  Conservative   16;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          1 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58
              |:| |||:||: ||  :  || |:  |::     ||  |||| |    ||||| |:| : |
Db         24 QDWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 79

Qy         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         80 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 127
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Qy          60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
               ||||||||||||||||||||||||||| |||||||||||||||||||||
Db          83 LSTTRFQLNTCTRTSITPRPCPYSSRTENNYICVKCENQYPVHFAGIGRCP 133


RESULT 2
Q98SM2
ID   Q98SM2      PRELIMINARY;      PRT;   132 AA.
AC   Q98SM2;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21539506; PubMed=11683320;
RA   Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT   "Rapid diversification of RNase A superfamily ribonuclease from the
RT   bullfrog, Rana catesbeiana.";
RL   J. Mol. Evol. 53:31-38(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Tang P.-C., Jeng J.-T.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF351207; AAK30253.1; -.
DR   EMBL; AF359578; AAL87036.1; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL       1     22       POTENTIAL.
FT   CHAIN       23    132       RC-RNASE7.
SQ   SEQUENCE   132 AA;  14412 MW;  131A745187978687 CRC64;

  Query Match             80.6%;  Score 483.5;  DB 13;  Length 132;
  Best Local Similarity   82.7%;  Pred. No. 8.4e-48;
  Matches   91;  Conservative    6;  Mismatches   12;  Indels    1;  Gaps    1;

Qy           1 QNWATFQQKHIINTPII-CNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 59
               | || |||||| :|  | ||||:||||||||||||:|||||||||||||| || | ||
Db          23 QTWAKFQQKHIPSTSSINCNTIMDNNIYIVGGQCKKVNTFIISSATTVKAICNGVTNSNV 82

Qy          60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
               || |||||:|||||||||||||||: ||| ||||||| ||||||||:|
Db          83 LSPTRFQLDTCTRTSITPRPCPYSSKKETNKICVKCENQLPVHFAGIGKC 132


RESULT 3
Q98SL9
ID   Q98SL9      PRELIMINARY;      PRT;   133 AA.
AC   Q98SL9;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RNase A-type ribonuclease rc212 precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21539506; PubMed=11683320;
RA   Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT   "Rapid diversification of RNase A superfamily ribonuclease from the
RT   bullfrog, Rana catesbeiana.";
RL   J. Mol. Evol. 53:31-38(2001).
DR   EMBL; AF351210; AAK30256.1; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL       1     22       POTENTIAL.
SQ   SEQUENCE   133 AA;  14615 MW;  C8785B236B26E54E CRC64;

  Query Match             79.1%;  Score 474.5;  DB 13;  Length 133;
  Best Local Similarity   77.5%;  Pred. No. 9.2e-47;
  Matches   86;  Conservative   12;  Mismatches   12;  Indels    1;  Gaps    1;

Qy           1 QNWATFQQKHIINTPII-CNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 59
               |||||||||| ||  | |: |::|::|||||||:|||| |||||| ||:|| :  |
Db          23 QNWATFQQKHITNTSSINCSNIMNNSLYIVGGQCKKVNTFIASSATTVKGICSGVTDKKV 82

Qy          60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
               ||:|:|||: |||  ||||||||||||||||||||||||||||:||
Db          83 LSSTKFQLDICTRIFITPRPCPYSSRTETNYICVKCENQYPVHFAGIGQCP 133


RESULT 4
Q98SL8
ID   Q98SL8      PRELIMINARY;      PRT;   133 AA.
AC   Q98SL8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RNase A-type ribonuclease rc218 precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21539506; PubMed=11683320;
RA   Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT   "Rapid diversification of RNase A superfamily ribonuclease from the
RT   bullfrog, Rana catesbeiana.";
RL   J. Mol. Evol. 53:31-38(2001).
DR   EMBL; AF351211; AAK30257.1; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL       1     22       POTENTIAL.
SQ   SEQUENCE   133 AA;  14590 MW;  8B40B9A94FA5B943 CRC64;

  Query Match             77.9%;  Score 467.5;  DB 13;  Length 133;
  Best Local Similarity   75.7%;  Pred. No. 5.9e-46;
  Matches   84;  Conservative   14;  Mismatches   12;  Indels    1;  Gaps    1;

Qy           1 QNWATFQQKHIINTPII-CNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 59
               |||||||::|| ||  | |: |::|::|||||||:|||| |||||| ||:|| :  |
Db          23 QNWATFQEQHITNTSSINCSNIMNNSLYIVGGQCKKVNTFIASSATTVKGICSGVTDKKV 82

Qy          60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
               ||:|:|||: |||  ||||||||||||||||||||||||||||:||
Db          83 LSSTKFQLDICTRIFITPRPCPYSSRTETNYICVKCENQYPVHFAGIGQCP 133
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:10 ; Search time 31.2816 Seconds
(without alignments)
1109.503 Million cell updates/sec

Title: US-09-961-400-19
Perfect score: 600
Sequence: 1 QNWATFQQKHIINTPIICNT.....ICVKCENQYPVHFAGIGRCP 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	554.5	92.4	133	13	Q98SM0	Q98sm0 rana catesb
2	483.5	80.6	132	13	Q98SM2	Q98sm2 rana catesb
3	474.5	79.1	133	13	Q98SL9	Q98sl9 rana catesb
4	467.5	77.9	133	13	Q98SL8	Q98sl8 rana catesb
5	444.5	74.1	132	13	Q98SM1	Q98sm1 rana catesb
6	372	62.0	132	13	Q9DF78	Q9df78 rana catesb
7	277.5	46.2	127	13	Q9I8V8	Q9i8v8 rana pipien
8	273.5	45.6	127	13	Q8UVX5	Q8uvx5 rana pipien
9	243	40.5	129	13	Q9DFY6	Q9dfy6 rana catesb
10	225.5	37.6	128	13	Q9DFY8	Q9dfy8 rana catesb
11	223.5	37.2	128	13	Q9DFY7	Q9dfy7 rana catesb
12	214.5	35.8	128	13	Q9DFY5	Q9dfy5 rana catesb
13	161	26.8	169	13	Q9W738	Q9w738 xenopus lae
14	128	21.3	170	6	Q9BEC1	Q9bec1 tragulus ja
15	127.5	21.2	144	11	Q80Z85	Q80z85 mus musculu
16	127.5	21.2	153	11	Q80XS4	Q80xs4 mus musculu
17	123.5	20.6	147	6	Q7YRJ6	Q7yrj6 balaena mys
18	122	20.3	146	6	Q861Y5	Q861y5 colobus gue
19	121.5	20.2	116	6	Q9TVC0	Q9tvc0 sus scrofa
20	121.5	20.2	163	6	Q9BDC2	Q9bdc2 antilocapra
21	121	20.2	150	11	Q8VD94	Q8vd94 berylmys bo
22	119	19.8	150	11	Q8VD88	Q8vd88 rattus norv
23	118.5	19.8	144	6	Q9BH14	Q9bh14 antilocapra
24	118.5	19.8	147	6	Q7YRJ5	Q7yrj5 tursiops tr
25	116.5	19.4	149	11	Q8K2T2	Q8k2t2 mus musculu
26	116.5	19.4	149	11	Q8C6G3	Q8c6g3 mus musculu
27	116	19.3	146	6	Q861Y4	Q861y4 trachypithe
28	116	19.3	150	11	Q8VD92	Q8vd92 rattus exul
29	115	19.2	146	6	Q861Y3	Q861y3 pygathrix r
30	115	19.2	146	6	Q861Y2	Q861y2 pygathrix b
31	115	19.2	146	6	Q861Y1	Q861y1 pygathrix a
32	113.5	18.9	152	11	Q8VD89	Q8vd89 rattus norv
33	111	18.5	148	11	Q8C663	Q8c663 mus musculu
34	110.5	18.4	124	6	Q95NE6	Q95ne6 bubalus bub
35	109.5	18.2	148	11	Q8C7E4	Q8c7e4 mus musculu
36	109.5	18.2	149	11	Q8VD95	Q8vd95 berylmys bo
37	109	18.2	124	6	Q9BEC2	Q9bec2 tragulus ja
38	109	18.2	134	6	Q9BDB9	Q9bdb9 tragulus ja
39	108.5	18.1	152	11	Q8VD84	Q8vd84 rattus tiom
40	108.5	18.1	156	6	Q8SQ05	Q8sq05 lagothrix l
41	107.5	17.9	119	6	Q9TV28	Q9tv28 eulemur ful
42	107.5	17.9	119	6	Q9TV30	Q9tv30 saguinus oe
43	106.5	17.8	156	6	Q8SQ06	Q8sq06 ateles geof
44	105.5	17.6	142	6	Q9BEC3	Q9bec3 tragulus ja
45	105.5	17.6	156	6	Q8SQ08	Q8sq08 saimiri sci

ALIGNMENTS

RESULT 1
Q98SM0
ID Q98SM0 PRELIMINARY; PRT; 133 AA.
AC Q98SM0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RNase A-type ribonuclease rc208 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351209; AAK30255.1; -.
DR HSSP; P11916; 1BC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNAse_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 22 POTENTIAL.
SQ SEQUENCE 133 AA; 14628 MW; 87FCF122C3499E02 CRC64;

Query Match 92.4%; Score 554.5; DB 13; Length 133;
Best Local Similarity 92.8%; Pred. No. 5.6e-56;
Matches 103; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

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Qy          1 QNWATFQQKHIINTPII-CNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 59
              ||||||||||| ||  | ||||:|||||||||||| |||||||||||||||||||:||
Db         23 QNWATFQQKHITNTSSINCNTIMDNNIYIVGGQCKGVNTFIISSATTVKAICTGVINMNV 82
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Q9BEC1
ID   Q9BEC1      PRELIMINARY;      PRT;   170 AA.
AC   Q9BEC1;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Brain-type ribonuclease ribonuclease precursor (Fragment).
GN   RNASE B.
OS   Tragulus javanicus (Lesser Malay chevrotain).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Tragulina;
OC   Tragulidae; Tragulus.
OX   NCBI_TaxID=9849;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21347458; PubMed=11453981;
RA   Breukelman H.J., Jekel P.A., Dubois J.Y., Mulder P.P.M.F.A.,
RA   Warmels H.W., Beintema J.J.;
RT   "Secretory ribonucleases in the primitive ruminant chevrotain
RT   (Tragulus javanicus).";
RL   Eur. J. Biochem. 268:3890-3897(2001).
CC   -!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR   EMBL; AJ271299; CAC24723.1; -.
DR   HSSP; P00656; 1LSQ.
DR   GO; GO:0004519; F:endonuclease activity; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Endonuclease; Hydrolase; Nuclease; Signal.
FT   NON_TER       1      1
FT   SIGNAL       <1     19       POTENTIAL.
FT   CHAIN        20    170       BRAIN-TYPE RIBONUCLEASE RIBONUCLEASE.
SQ   SEQUENCE   170 AA;  18832 MW;  AB6CE7E1E5549AA0 CRC64;

  Query Match             21.6%;  Score 131;  DB 6;  Length 170;
  Best Local Similarity   33.1%;  Pred. No. 2.9e-07;
  Matches   41;  Conservative   17;  Mismatches   46;  Indels   20;  Gaps    7;

Qy          5 ATFQQKHI------INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICT----- 53
              | |:::|:      ||:   || :|     :  |:|| |||||  |   |||||:
Db         25 AKFRRQHLDAGNSSINSN-YCNLMMKRR-KMTHGRCKPVNTFIHESLEDVKAICSEKNIT 82

Qy         54 ---GVINMNVLSTTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCEN--QYPVHFAGI 107
                 |  | :  ::|   :  | :|  :  | | | :  :  || | ||     |||| |
Db         83 CKNGQPNCHQSNST-MNITDCRQTGGSKYPNCAYKTSQKQKYIIVACEGTPSVPVHFDGS 141

Qy        108 GRCP 111
                |
Db        142 AVLP 145


RESULT 15
Q80Z85
ID   Q80Z85      PRELIMINARY;      PRT;   144 AA.
AC   Q80Z85;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Angiogenin-4.
GN   ANG4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NMRI;
RX   MEDLINE=22493143; PubMed=12548285;
RA   Hooper L.V., Stappenbeck T.S., Hong C.V., Gordon J.I.;
RT   "Angiogenins: a new class of microbicidal proteins involved in innate
RT   immunity.";
RL   Nat. Immunol. 4:269-273(2003).
DR   EMBL; AY219870; AAO62354.1; -.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
SQ   SEQUENCE   144 AA;  16554 MW;  09808807C00224C1 CRC64;

  Query Match             21.2%;  Score 128.5;  DB 11;  Length 144;
  Best Local Similarity   38.2%;  Pred. No. 4.7e-07;
  Matches   29;  Conservative   13;  Mismatches   29;  Indels    5;  Gaps    3;

Qy         34 CKRVNTFIISSATTVKAIC---TGVINMNV-LSTTRFQLNTCTRTSITP-RPCPYSSRTE 88
              || |||||  :   ::|||      |  :| : ||: ||| :  :|  || | :  :
Db         62 CKDVNTFIHGTKKNIRAICGKKGSPYGENFRISNSPFQITTCTHSRGSPWPPCGYRAFKD 121

Qy         89 TNYICVKCENQYPVHF 104
                || : ||: :||||
Db        122 FRYIVIACEDGWPVHF 137


Search completed: May  7, 2004, 21:46:04
Job time : 32.5659 secs
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RESULT 11
Q9DFY7
ID   Q9DFY7      PRELIMINARY;      PRT;   128 AA.
AC   Q9DFY7;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RC-RNase3 ribonuclease precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20512555; PubMed=11058105;
RA   Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT   "Purification and cloning of cytotoxic ribonucleases from Rana
RT   catesbeiana (bullfrog).";
RL   Nucleic Acids Res. 28:4097-4104(2000).
DR   EMBL; AF242554; AAG31440.2; -.
DR   HSSP; P22069; 1ONC.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24    128       RC-RNASE3 RIBONUCLEASE.
SQ   SEQUENCE   128 AA;  14517 MW;  2B14986082E0587D CRC64;

  Query Match             37.3%;  Score 226.5;  DB 13;  Length 128;
  Best Local Similarity   41.1%;  Pred. No. 1.6e-18;
  Matches   46;  Conservative   18;  Mismatches   39;  Indels    9;  Gaps    4;

Qy          2 QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGV-INMN 59
              |:| |||:||: :|  : |:  |   ::     ||: |||| :    |||:|  :  | :
Db         24 QDWETFQKKHLTDTKKVKCDVEMAKALF----DCKKTNTFIYALPGRVKALCKNIRDNTD 79

Qy         60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
              |||   | |  | |  :   || |   : || ||: | || |:||||:| ||
Db         80 VLSRDAFLLPQCDRIKL---PCHYKLSSSTNTICITCVNQLPIHFAGVGSCP 128


RESULT 12
Q9DFY5
ID   Q9DFY5      PRELIMINARY;      PRT;   128 AA.
AC   Q9DFY5;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RC-RNase6 ribonuclease precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20512555; PubMed=11058105;
RA   Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT   "Purification and cloning of cytotoxic ribonucleases from Rana
RT   catesbeiana (bullfrog).";
RL   Nucleic Acids Res. 28:4097-4104(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF242556; AAG31442.2; -.
DR   HSSP; P22069; 1ONC.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24    128       RC-RNASE6 RIBONUCLEASE.
SQ   SEQUENCE   128 AA;  14804 MW;  AFEBFD67D266C7C2 CRC64;

  Query Match             35.8%;  Score 217.5;  DB 13;  Length 128;
  Best Local Similarity   39.3%;  Pred. No. 1.7e-17;
  Matches   44;  Conservative   19;  Mismatches   40;  Indels    9;  Gaps    4;

Qy          2 QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGV-INMN 59
              |:| |||:||: :|  : |:  |   ::     ||: |||| :    |:|:|  :  | |
Db         24 QDWDTFQKKHLTDTKKVKCDVEMKKALF----DCKKTNTFIFARPPRVQALCKNIKDNTN 79

Qy         60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
              |||   | |  | |  :   || |    || ||: |  : |:||||:|:||
Db         80 VLSRDVFYLPQCNRKKL---PCHYRLDGSTNTICLTCMKELPIHFAGVGKCP 128


RESULT 13
Q9W738
ID   Q9W738      PRELIMINARY;      PRT;   169 AA.
AC   Q9W738;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   FRL2 protein.
GN   FRL2.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96069863; PubMed=7585965;
RA   Kinoshita N., Minshull J., Kirschner M.W.;
RT   "The identification of two novel ligands of the FGF receptor by a
RT   yeast screening method and their activity in Xenopus development.";
RL   Cell 83:621-630(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Kinoshita N., Kirschner M.W.;
RL   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF159166; AAD41901.1; -.
DR   HSSP; P00656; 1LSQ.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
SQ   SEQUENCE   169 AA;  18891 MW;  D969F3E43B3CE1B8 CRC64;

  Query Match             26.9%;  Score 163;  DB 13;  Length 169;
  Best Local Similarity   39.3%;  Pred. No. 5.3e-11;
  Matches   44;  Conservative   10;  Mismatches   50;  Indels    8;  Gaps    6;

Qy          2 QNWATFQQKHII--NTPIICN-TIMDNNIYIVGGQCKRVNTFI-ISSATTVKAICTGVIN 57
              ||    | :|||:       || || | ||      ||  ||||  ::   || :| |::
Db         28 QNINAFMEKHIVKEGAETNCNQTIKDRNIRF-KNNCKFRNTFIHDTNGKKVKEMCAGIVK 86

Qy         58 MN-VLSTTRFQLNTCTRTSITPRP--CPYSSRTETNYICVKCENQYPVHFAG 106
              |:|     |  |      | ||  | |:    |  | : ||| |||||||
Db         87 STFVISKELLPLTDCLLMGRTARPPNCAYNQTRTTGVINITCENNYPVHFAG 138


RESULT 14
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RESULT 8
Q8UVX5
ID   Q8UVX5      PRELIMINARY;      PRT;   127 AA.
AC   Q8UVX5;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Onconase precursor.
GN   RPR.
OS   Rana pipiens (Northern leopard frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8404;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Liao Y.-D., Wang S.-C.;
RT   "Rana pipiens onconase genomic DNA.";
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF332139; AAL54383.1; -.
DR   PIR; A39035; A39035.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     23       POTENTIAL.
SQ   SEQUENCE   127 AA;  14469 MW;  953F90D351CFEEF3 CRC64;

  Query Match             45.7%;  Score 277.5;  DB 13;  Length 127;
  Best Local Similarity   49.5%;  Pred. No. 1.7e-24;
  Matches   55;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          2 QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 59
              |:| |||:||| ||  : |: ||  |::     ||  |||| |    ||||| |:| : |
Db         24 QDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 79

Qy         60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         80 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 127


RESULT 9
Q9DFY6
ID   Q9DFY6      PRELIMINARY;      PRT;   129 AA.
AC   Q9DFY6;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RC-RNase4 ribonuclease precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20512555; PubMed=11058105;
RA   Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT   "Purification and cloning of cytotoxic ribonucleases from Rana
RT   catesbeiana (bullfrog).";
RL   Nucleic Acids Res. 28:4097-4104(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF242555; AAG31441.2; -.
DR   PDB; 1KVZ; 28-JUL-02.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24    129       RC-RNASE4 RIBONUCLEASE.
SQ   SEQUENCE   129 AA;  14724 MW;  826A62882B10ABDA CRC64;

  Query Match             40.5%;  Score 246;  DB 13;  Length 129;
  Best Local Similarity   43.4%;  Pred. No. 8.4e-21;
  Matches   49;  Conservative   24;  Mismatches   30;  Indels   10;  Gaps    5;

Qy          2 QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 59
              |:||||::||: :|  : |: :|  :::     ||  |||| |    |||:| ||| : :
Db         24 QDWATFKKKHLTDTWDVDCDNLMPTSLF----DCKDKNTFIYSLPGPVKALCRGVIFSAD 79

Qy         60 VLSTTRFQLNTCTRTSITPR-PCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
              ||| : | |  |   :: || || |  :  :| ||::||:: ||||||:| ||
Db         80 VLSNSEFYLAEC---NVKPRKPCKYKLKKSSNRICIRCEHELPVHFAGVGICP 129


RESULT 10
Q9DFY8
ID   Q9DFY8      PRELIMINARY;      PRT;   128 AA.
AC   Q9DFY8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RC-RNase2 ribonuclease precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20512555; PubMed=11058105;
RA   Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT   "Purification and cloning of cytotoxic ribonucleases from Rana
RT   catesbeiana (bullfrog).";
RL   Nucleic Acids Res. 28:4097-4104(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF242553; AAG31439.1; -.
DR   PDB; 1M58; 09-JAN-03.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24    128       RC-RNASE2 RIBONUCLEASE.
SQ   SEQUENCE   128 AA;  14839 MW;  989719CF52053ECC CRC64;

  Query Match             37.8%;  Score 229.5;  DB 13;  Length 128;
  Best Local Similarity   40.2%;  Pred. No. 7e-19;
  Matches   45;  Conservative   20;  Mismatches   38;  Indels    9;  Gaps    4;

Qy          2 QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 59
              ||| |||:||: :|  : |:  |   ::     ||: |||| :    |:|:|  :| : |
Db         24 QNWETFQKKHLTDTRDVKCDAEMKKALF----DCKQKNTFIYARPGRVQALCKNIIVSKN 79

Qy         60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
              ||||  | |: | |  :   || |  :  :| ||: |||: ||||  :  ||
Db         80 VLSTDEFYLSDCNRIKL---PCHYKLKKSSNTICITCENKLPVHFVAVEECP 128
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RESULT 5
Q98SM1
ID   Q98SM1      PRELIMINARY;      PRT;   132 AA.
AC   Q98SM1;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RNase A-type ribonuclease rc204 precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21539506; PubMed=11683320;
RA   Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT   "Rapid diversification of RNase A superfamily ribonuclease from the
RT   bullfrog, Rana catesbeiana.";
RL   J. Mol. Evol. 53:31-38(2001).
DR   EMBL; AF351208; AAK30254.1; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     22       POTENTIAL.
SQ   SEQUENCE   132 AA;  14704 MW;  95D61760F729868E CRC64;

  Query Match             73.9%;  Score 448.5;  DB 13;  Length 132;
  Best Local Similarity   78.2%;  Pred. No. 2.1e-44;
  Matches   86;  Conservative    7;  Mismatches   16;  Indels    1;  Gaps    1;

Qy          2 QNWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60
              |:| ||||||| :|  | |||||| :|||| ||||:|||||| ||||||||||||:| ||
Db         23 QDWPTFQQKHIPSTSSIDCNTIMDKDIYIVRGQCKKVNTFIIYSATTVKAICTGVLNSNV 82

Qy         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              |||||||   ||| || |||||||  ||| |||||||:|||||||:|
Db         83 LSTTRFQLXXXTRTFITSRPCPYSSTKETNKICVKCENEYPVHFAGIGKC 132


RESULT 6
Q9DF78
ID   Q9DF78      PRELIMINARY;      PRT;   132 AA.
AC   Q9DF78;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RC-RNaseL1 ribonuclease precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20512555; PubMed=11058105;
RA   Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT   "Purification and cloning of cytotoxic ribonucleases from Rana
RT   catesbeiana (bullfrog).";
RL   Nucleic Acids Res. 28:4097-4104(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF288642; AAG30414.2; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    132       RC-RNASEL1 RIBONUCLEASE.
SQ   SEQUENCE   132 AA;  14625 MW;  D8D9A517452FBE53 CRC64;

  Query Match             61.9%;  Score 376;  DB 13;  Length 132;
  Best Local Similarity   65.8%;  Pred. No. 5.9e-36;
  Matches   73;  Conservative    9;  Mismatches   27;  Indels    2;  Gaps    2;

Qy          2 QNWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 59
              |||| |::||| :|  | |||||| ||||||:|| ||||||| |||||:||  :
Db         22 QNWAKFKEKHITSTSSIDCNTIMDKAIYIVGGKCKERNTFIISSEDNVKAICSGVSPDRK 81

Qy         60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              |||| |:|||| | |||||||||    : | |||||| | |||| |||:|
Db         82 ELSTTSFKLNTCIRDSITPRPCPYHPSPDNNKICVKCEKQLPVHFVGIGKC 132


RESULT 7
Q9I8V8
ID   Q9I8V8      PRELIMINARY;      PRT;   127 AA.
AC   Q9I8V8;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Onconase variant rapLR1 precursor.
OS   Rana pipiens (Northern leopard frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8404;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20330357; PubMed=10871370;
RA   Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;
RT   "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a
RT   3' UTR of unusual length and structure.";
RL   Nucleic Acids Res. 28:2375-2382(2000).
DR   EMBL; AF165133; AAF76935.1; -.
DR   PIR; A39035; A39035.
DR   HSSP; P22069; 1ONC.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     23       POTENTIAL.
SQ   SEQUENCE   127 AA;  14491 MW;  B8511DC5407AB69B CRC64;

  Query Match             46.4%;  Score 281.5;  DB 13;  Length 127;
  Best Local Similarity   49.5%;  Pred. No. 6e-25;
  Matches   55;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          2 QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 59
              |:| |||:||: ||  : || ||  |::     ||  |||| |    ||||| |:| : |
Db         24 QDWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 79

Qy         60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         80 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 127
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Qy          61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
               ||||||||||||||||||||||||||| |||||||||||||||||||||
Db          83 LSTTRFQLNTCTRTSITPRPCPYSSRTENNYICVKCENQYPVHFAGIGRCP 133


RESULT 2
Q98SM2
ID   Q98SM2      PRELIMINARY;      PRT;   132 AA.
AC   Q98SM2;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21539506; PubMed=11683320;
RA   Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT   "Rapid diversification of RNase A superfamily ribonuclease from the
RT   bullfrog, Rana catesbeiana.";
RL   J. Mol. Evol. 53:31-38(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Tang P.-C., Jeng J.-T.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF351207; AAK30253.1; -.
DR   EMBL; AF359578; AAL87036.1; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     22       POTENTIAL.
FT   CHAIN        23    132       RC-RNASE7.
SQ   SEQUENCE   132 AA;  14412 MW;  131A745187978687 CRC64;

  Query Match             80.3%;  Score 487.5;  DB 13;  Length 132;
  Best Local Similarity   83.6%;  Pred. No. 5.9e-49;
  Matches   92;  Conservative    5;  Mismatches   12;  Indels    1;  Gaps    1;

Qy           2 QNWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60
               | || |||||| :|  | |||||||||||||||:||||||||||||| || | ||
Db          23 QTWAKFQQKHIPSTSSINCNTIMDNNIYIVGGQCKKVNTFIISSATTVKAICNGVTNSNV 82

Qy          61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
               || |||||:|||||||||||||||: ||| |||||||| |||||||:|
Db          83 LSPTRFQLDTCTRTSITPRPCPYSSKKETNKICVKCENQLPVHFAGIGKC 132


RESULT 3
Q98SL9
ID   Q98SL9      PRELIMINARY;      PRT;   133 AA.
AC   Q98SL9;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RNase A-type ribonuclease rc212 precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21539506; PubMed=11683320;
RA   Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT   "Rapid diversification of RNase A superfamily ribonuclease from the
RT   bullfrog, Rana catesbeiana.";
RL   J. Mol. Evol. 53:31-38(2001).
DR   EMBL; AF351210; AAK30256.1; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     22       POTENTIAL.
SQ   SEQUENCE   133 AA;  14615 MW;  C8785B236B26E54E CRC64;

  Query Match             78.8%;  Score 478.5;  DB 13;  Length 133;
  Best Local Similarity   78.4%;  Pred. No. 6.7e-48;
  Matches   87;  Conservative   11;  Mismatches   12;  Indels    1;  Gaps    1;

Qy           2 QNWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60
               |||||||||| ||  | |: ||:|::||||||||:|||| ||||||| ||:|| :  |
Db          23 QNWATFQQKHITNTSSINCSNIMNNSLYIVGGQCKKVNTFIASSATTVKGICSGVTDKKV 82

Qy          61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
               ||:|:|||: |||  |||||||||||||||||||||||||||||:||
Db          83 LSSTKFQLDICTRIFITPRPCPYSSRTETNYICVKCENQYPVHFAGIGQCP 133


RESULT 4
Q98SL8
ID   Q98SL8      PRELIMINARY;      PRT;   133 AA.
AC   Q98SL8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RNase A-type ribonuclease rc218 precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21539506; PubMed=11683320;
RA   Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT   "Rapid diversification of RNase A superfamily ribonuclease from the
RT   bullfrog, Rana catesbeiana.";
RL   J. Mol. Evol. 53:31-38(2001).
DR   EMBL; AF351211; AAK30257.1; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     22       POTENTIAL.
SQ   SEQUENCE   133 AA;  14590 MW;  8B40B9A94FA5B943 CRC64;

  Query Match             77.7%;  Score 471.5;  DB 13;  Length 133;
  Best Local Similarity   76.6%;  Pred. No. 4.4e-47;
  Matches   85;  Conservative   13;  Mismatches   12;  Indels    1;  Gaps    1;

Qy           2 QNWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60
               |||||||::|| ||  | |: ||:|::||||||||:|||| ||||||| ||:|| :  |
Db          23 QNWATFQEQHITNTSSINCSNIMNNSLYIVGGQCKKVNTFIASSATTVKGICSGVTDKKV 82

Qy          61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
               ||:|:|||: |||  |||||||||||||||||||||||||||||:||
Db          83 LSSTKFQLDICTRIFITPRPCPYSSRTETNYICVKCENQYPVHFAGIGQCP 133
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:10 ; Search time 31.566 Seconds
(without alignments)
1109.503 Million cell updates/sec

Title: US-09-961-400-17
Perfect score: 607
Sequence: 1 MQNWATFQQKHIINTPIICN.....ICVKCENQYPVHFAGIGRCP 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	560.5	92.3	133	13	Q98SM0	Q98sm0 rana catesb
2	487.5	80.3	132	13	Q98SM2	Q98sm2 rana catesb
3	478.5	78.8	133	13	Q98SL9	Q98sl9 rana catesb
4	471.5	77.7	133	13	Q98SL8	Q98sl8 rana catesb
5	448.5	73.9	132	13	Q98SM1	Q98sm1 rana catesb
6	376	61.9	132	13	Q9DF78	Q9df78 rana catesb
7	281.5	46.4	127	13	Q9I8V8	Q9i8v8 rana pipien
8	277.5	45.7	127	13	Q8UVX5	Q8uvx5 rana pipien
9	246	40.5	129	13	Q9DFY6	Q9dfy6 rana catesb
10	229.5	37.8	128	13	Q9DFY8	Q9dfy8 rana catesb
11	226.5	37.3	128	13	Q9DFY7	Q9dfy7 rana catesb
12	217.5	35.8	128	13	Q9DFY5	Q9dfy5 rana catesb
13	163	26.9	169	13	Q9W738	Q9w738 xenopus lae
14	131	21.6	170	6	Q9BEC1	Q9bec1 tragulus ja
15	128.5	21.2	144	11	Q8Z085	Q80z85 mus musculu
16	128.5	21.2	153	11	Q80XS4	Q80xs4 mus musculu
17	127.5	21.0	147	6	Q7YRJ6	Q7yrj6 balaena mys
18	126	20.8	150	11	Q8VD94	Q8vd94 berylmys bo
19	125.5	20.7	163	6	Q9BDC2	Q9bdc2 antilocapra
20	124.5	20.5	116	6	Q9TVC0	Q9tvc0 sus scrofa
21	124	20.4	150	11	Q8VD88	Q8vd88 rattus norv
22	122.5	20.2	144	6	Q9BH14	Q9bh14 antilocapra
23	121.5	20.0	147	6	Q7YRJ5	Q7yrj5 tursiops tr
24	121	19.9	146	6	Q861Y5	Q861y5 colobus gue
25	120.5	19.9	149	11	Q8K2T2	Q8k2t2 mus musculu
26	120.5	19.9	149	11	Q8C6G3	Q8c6g3 mus musculu
27	120	19.8	150	11	Q8VD92	Q8vd92 rattus exul
28	119.5	19.7	146	6	Q861Y4	Q861y4 trachypithe
29	118.5	19.5	146	6	Q861Y3	Q861y3 pygathrix r
30	118.5	19.5	146	6	Q861Y2	Q861y2 pygathrix b
31	118.5	19.5	146	6	Q861Y1	Q861y1 pygathrix a
32	116.5	19.2	152	11	Q8VD89	Q8vd89 rattus norv
33	114.5	18.9	124	6	Q95NE6	Q95ne6 bubalus bub
34	112.5	18.5	148	11	Q8C7E4	Q8c7e4 mus musculu
35	112.5	18.5	149	11	Q8VD95	Q8vd95 berylmys bo
36	112	18.5	134	6	Q9BDB9	Q9bdb9 tragulus ja
37	111.5	18.4	152	11	Q8VD84	Q8vd84 rattus tiom
38	111.5	18.4	156	6	Q8SQ05	Q8sq05 lagothrix l
39	111	18.3	148	11	Q8C663	Q8c663 mus musculu
40	110.5	18.2	119	6	Q9TV28	Q9tv28 eulemur ful
41	110.5	18.2	119	6	Q9TV30	Q9tv30 saguinus oe
42	109.5	18.0	142	6	Q9BEC3	Q9bec3 tragulus ja
43	109.5	18.0	156	6	Q8SQ06	Q8sq06 ateles geof
44	109	18.0	124	6	Q9BEC2	Q9bec2 tragulus ja
45	108.5	17.9	156	6	Q8SQ08	Q8sq08 saimiri sci

ALIGNMENTS

RESULT 1
Q98SM0
ID Q98SM0 PRELIMINARY; PRT; 133 AA.
AC Q98SM0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RNase A-type ribonuclease rc208 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351209; AAK30255.1; -.
DR HSSP; P11916; 1BC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNAse_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 22 POTENTIAL.
SQ SEQUENCE 133 AA; 14628 MW; 87FCF122C3499E02 CRC64;

Query Match 92.3%; Score 560.5; DB 13; Length 133;
Best Local Similarity 94.6%; Pred. No. 1.8e-57;
Matches 105; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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Qy          2 QNWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60
              |||||||||| ||  | |||||||||||||||| ||||||||||||||||||||||||
Db         23 QNWATFQQKHITNTSSINCNTIMDNNIYIVGGQCKGVNTFIISSATTVKAICTGVINMNV 82
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Q9JKI5
ID   Q9JKI5      PRELIMINARY;      PRT;   152 AA.
AC   Q9JKI5;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Eosinophil-associated ribonuclease 10.
GN   EAR10.
OS   Mus saxicola (Spiny mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10094;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20243759; PubMed=10758160;
RA   Zhang J., Dyer K.D., Rosenberg H.F.;
RT   "Evolution of the rodent eosinophil-associated ribonuclease gene
RT   family by rapid gene sorting and positive selection.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:4701-4706(2000).
DR   EMBL; AF238398; AAF67698.1; -.
DR   HSSP; P10153; 1HI2.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
SQ   SEQUENCE   152 AA;  16830 MW;  780421C3661732C8 CRC64;

  Query Match             22.9%;  Score 133;  DB 11;  Length 152;
  Best Local Similarity   30.3%;  Pred. No. 2e-07;
  Matches   37;  Conservative   19;  Mismatches   42;  Indels   24;  Gaps    6;

Qy          2 SDWLTFQKKHLTNTRDVDCNNIM---STNLFHCKDKNTFIYSRPEPVKAIC---KGIIA- 54
              | |   |  :|:||| :  ||  |   : |   ||: |||:::    |  :|    |: :
Db         31 SQW--FATQHITNTANPQCNVEMLPINRNRTRCKNINTFLHTHFANVVGVCGNPSGLCSN 88

Qy         55 --SKNVLTTSEFYLSDCNVTSR-----PCKYKLKKSTNTFCVTCENQAP--------VHF 99
                | |    :|   :: ||:|||       |:|: | |   : | |  : |         ||
Db         89 NISTNCHNSSRVPITVCNITSREKSCTQCRYQTKGSVEYYTVACNPRTPQDSPRYPVVHL 148

Qy        100 VG 101
               |
Db        149 DG 150


RESULT 15
Q9JKI9
ID   Q9JKI9      PRELIMINARY;      PRT;   157 AA.
AC   Q9JKI9;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Eosinophil-associated ribonuclease 44.
GN   EAR44.
OS   Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC   Meriones.
OX   NCBI_TaxID=10047;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20243759; PubMed=10758160;
RA   Zhang J., Dyer K.D., Rosenberg H.F.;
RT   "Evolution of the rodent eosinophil-associated ribonuclease gene
RT   family by rapid gene sorting and positive selection.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:4701-4706(2000).
DR   EMBL; AF238394; AAF67694.1; -.
DR   HSSP; P10153; 1HI2.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
SQ   SEQUENCE   157 AA;  17887 MW;  34FE2AE777EF3709 CRC64;

  Query Match             22.5%;  Score 131;  DB 11;  Length 157;
  Best Local Similarity   30.6%;  Pred. No. 3.5e-07;
  Matches   34;  Conservative   20;  Mismatches   37;  Indels   20;  Gaps    7;

Qy          2 SDWLTFQKKHLTNTRDVDCNNIM-STNLF--HCKDKNTFIYSRPEPV-------KAICKG 51
              | | | |  |::||  : ||  |   | :   ||| |||:::|   |          ||
Db         34 SQWFTIQ--HISNTTTIQCNAAMLGVNNYTGRCKDLNTFLHTRFANVVNECYNRNTTCKN 91

Qy         52 IIASKNVL-TTSEFYLSDCNVTS-----RPCKYKLKKSTNTFCVTCENQAP 96
                :|   : |:  ::|||:||      | |:|:  ::   : : | |: |
Db         92 --GRRNCHDSRSKVSITDCNLTSPSANYRQCRYQRTRARKFYRIACNNKTP 140


Search completed: May  7, 2004, 21:46:03
Job time : 30.8597 secs
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RESULT 11
Q98SM1
ID   Q98SM1      PRELIMINARY;      PRT;   132 AA.
AC   Q98SM1;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RNase A-type ribonuclease rc204 precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21539506; PubMed=11683320;
RA   Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT   "Rapid diversification of RNase A superfamily ribonuclease from the
RT   bullfrog, Rana catesbeiana.";
RL   J. Mol. Evol. 53:31-38(2001).
DR   EMBL; AF351208; AAK30254.1; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     22       POTENTIAL.
SQ   SEQUENCE   132 AA;  14704 MW;  95D61760F729868E CRC64;

  Query Match             47.3%;  Score 275;  DB 13;  Length 132;
  Best Local Similarity   48.2%;  Pred. No. 7.2e-24;
  Matches   53;  Conservative   14;  Mismatches   35;  Indels    8;  Gaps    3;

Qy          3 DWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV 58
              || |||:||: :|  :||| ||  :::     ||  ||||      ||||| |:: | ||
Db         24 DWPTFQQKHIPSTSSIDCNTIMDKDIYIVRGQCKKVNTFIIYSATTVKAICTGVLNS-NV 82

Qy         59 LTTSEFYLSDCN---VTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
              |:|: | |       :||||| |   | ||  || |||: |||| |:| |
Db         83 LSTTRFQLXXXTRTFITSRPCPYSSTKETNKICVKCENEYPVHFAGIGKC 132


RESULT 12
Q9DF78
ID   Q9DF78      PRELIMINARY;      PRT;   132 AA.
AC   Q9DF78;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RC-RNaseL1 ribonuclease precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20512555; PubMed=11058105;
RA   Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT   "Purification and cloning of cytotoxic ribonucleases from Rana
RT   catesbeiana (bullfrog).";
RL   Nucleic Acids Res. 28:4097-4104(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF288642; AAG30414.2; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    132       RC-RNASEL1 RIBONUCLEASE.
SQ   SEQUENCE   132 AA;  14625 MW;  D8D9A517452FBE53 CRC64;

  Query Match             46.5%;  Score 270.5;  DB 13;  Length 132;
  Best Local Similarity   43.6%;  Pred. No. 2.4e-23;
  Matches   48;  Conservative   19;  Mismatches   36;  Indels    7;  Gaps    2;

Qy          3 DWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV 58
              :|  |::||:|:|  :||| ||   ::     ||::|||| |  : ||||| |:   :
Db         23 NWAKFKEKHITSTSSIDCNTIMDKAIYIVGGKCKERNTFIISSEDNVKAICSGVSPDRKE 82

Qy         59 LTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
              |:|: | |: |   ::| |||       |  || || | |||||:| |
Db         83 LSTTSFKLNTCIRDSITPRPCPYHPSPDNNKICVKCEKQLPVHFVGIGKC 132


RESULT 13
Q9W738
ID   Q9W738      PRELIMINARY;      PRT;   169 AA.
AC   Q9W738;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   FRL2 protein.
GN   FRL2.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96069863; PubMed=7585965;
RA   Kinoshita N., Minshull J., Kirschner M.W.;
RT   "The identification of two novel ligands of the FGF receptor by a
RT   yeast screening method and their activity in Xenopus development.";
RL   Cell 83:621-630(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Kinoshita N., Kirschner M.W.;
RL   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF159166; AAD41901.1; -.
DR   HSSP; P00656; 1LSQ.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
SQ   SEQUENCE   169 AA;  18891 MW;  D969F3E43B3CE1B8 CRC64;

  Query Match             27.1%;  Score 157.5;  DB 13;  Length 169;
  Best Local Similarity   36.1%;  Pred. No. 3.3e-10;
  Matches   39;  Conservative   19;  Mismatches   35;  Indels   15;  Gaps    6;

Qy          7 FQKKHLTNT-RDVDCN------NIMSTNLFHCKDKNTFIY-SRPEPVKAICKGIIASKNV 58
              | :||:     : :||      ||   |  :|| :||||: :  : || :| ||: |  |
Db         33 FMEKHIVKEGAETNCNQTIKDRNIRFKN--NCKFRNTFIHDTNGKKVKEMCAGIVKSTFV 90

Qy         59 LTTSEFYLSDCNV---TSRP--CKYKLKKSTNTFCVTCENQAPVHFVG 101
              ::     |:|| :   |:||  | |   ::|    :||||  |||| |
Db         91 ISKELLPLTDCLLMGRTARPPNCAYNQTRTTGVINITCENNYPVHFAG 138


RESULT 14
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                |:|: | |: |   ::| ||| |  :   |  || |||| |||| |:| |
Db         83 LSTTRFQLNTCTRTSITPRPCPYSSRTENNYICVKCENQYPVHFAGIGRC 132


RESULT 8
Q98SM2
ID   Q98SM2      PRELIMINARY;      PRT;   132 AA.
AC   Q98SM2;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21539506; PubMed=11683320;
RA   Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT   "Rapid diversification of RNase A superfamily ribonuclease from the
RT   bullfrog, Rana catesbeiana.";
RL   J. Mol. Evol. 53:31-38(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Tang P.-C., Jeng J.-T.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF351207; AAK30253.1; -.
DR   EMBL; AF359578; AAL87036.1; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     22       POTENTIAL.
FT   CHAIN        23    132       RC-RNASE7.
SQ   SEQUENCE   132 AA;  14412 MW;  131A745187978687 CRC64;

  Query Match             48.3%;  Score 281;  DB 13;  Length 132;
  Best Local Similarity   47.7%;  Pred. No. 1.5e-24;
  Matches   52;  Conservative   14;  Mismatches   35;  Indels    8;  Gaps    3;

Qy          4 WLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNVL 59
              |  ||:||: :|  ::|| ||  |::     ||  |||| |    ||||| | : : |||
Db         25 WAKFQQKHIPSTSSINCNTIMDNNIYIVGGQCKKVNTFIISSATTVKAICNG-VTNSNVL 83

Qy         60 TTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
              : : | |  |   ::| ||| |  || ||  || |||| |||| |:| |
Db         84 SPTRFQLDTCTRTSITPRPCPYSSKKETNKICVKCENQLPVHFAGIGKC 132


RESULT 9
Q98SL9
ID   Q98SL9      PRELIMINARY;      PRT;   133 AA.
AC   Q98SL9;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RNase A-type ribonuclease rc212 precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21539506; PubMed=11683320;
RA   Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT   "Rapid diversification of RNase A superfamily ribonuclease from the
RT   bullfrog, Rana catesbeiana.";
RL   J. Mol. Evol. 53:31-38(2001).
DR   EMBL; AF351210; AAK30256.1; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     22       POTENTIAL.
SQ   SEQUENCE   133 AA;  14615 MW;  C8785B236B26E54E CRC64;

  Query Match             48.3%;  Score 281;  DB 13;  Length 133;
  Best Local Similarity   47.3%;  Pred. No. 1.5e-24;
  Matches   52;  Conservative   17;  Mismatches   33;  Indels    8;  Gaps    3;

Qy          3 DWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV 58
              :| |||:|||:|||  ::|:|||: :|:     ||  |||| |    || || | :  | |
Db         24 NWATFQQKHITNTSSINCSNIMNNSLYIVGGQCKKVNTFIASSATTVKGICSG-VTDKKV 82

Qy         59 LTTSEFYLSDCN---VTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
              |::::| |  |    :| ||| |  :  ||  || |||| |||| |:| |
Db         83 LSSTKFQLDICTRIFITPRPCPYSSRTETNYICVKCENQYPVHFAGIGQC 132


RESULT 10
Q98SL8
ID   Q98SL8      PRELIMINARY;      PRT;   133 AA.
AC   Q98SL8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RNase A-type ribonuclease rc218 precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21539506; PubMed=11683320;
RA   Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT   "Rapid diversification of RNase A superfamily ribonuclease from the
RT   bullfrog, Rana catesbeiana.";
RL   J. Mol. Evol. 53:31-38(2001).
DR   EMBL; AF351211; AAK30257.1; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     22       POTENTIAL.
SQ   SEQUENCE   133 AA;  14590 MW;  8B40B9A94FA5B943 CRC64;

  Query Match             47.6%;  Score 277;  DB 13;  Length 133;
  Best Local Similarity   46.4%;  Pred. No. 4.3e-24;
  Matches   51;  Conservative   18;  Mismatches   33;  Indels    8;  Gaps    3;

Qy          3 DWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV 58
              :| |||::|:|||  ::|:|||: :|:     ||  |||| |    || || | :  | |
Db         24 NWATFQEQHITNTSSINCSNIMNNSLYIVGGQCKKVNTFIASSATTVKGICSG-VTDKKV 82

Qy         59 LTTSEFYLSDCN---VTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
              |::::| |  |    :| ||| |  :  ||  || |||| |||| |:| |
Db         83 LSSTKFQLDICTRIFITPRPCPYSSRTETNYICVKCENQYPVHFAGIGQC 132
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Db         25 NWETFQKKHLTDTRDVKCDAEMKKALFDCKQKNTFIYARPGRVQALCKNIIVSKNVLSTD 84

Qy         63 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
Db         85 EFYLSDCNRIKLPCHYKLKKSSNTICITCENKLPVHFVAVEEC 127


RESULT 5
Q9DFY7
ID   Q9DFY7      PRELIMINARY;      PRT;   128 AA.
AC   Q9DFY7;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RC-RNase3 ribonuclease precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20512555; PubMed=11058105;
RA   Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT   "Purification and cloning of cytotoxic ribonucleases from Rana
RT   catesbeiana (bullfrog).";
RL   Nucleic Acids Res. 28:4097-4104(2000).
DR   EMBL; AF242554; AAG31440.2; -.
DR   HSSP; P22069; 1ONC.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL       1     23       POTENTIAL.
FT   CHAIN       24    128       RC-RNASE3 RIBONUCLEASE.
SQ   SEQUENCE   128 AA;  14517 MW;  2B14986082E0587D CRC64;

  Query Match             52.6%;  Score 306;  DB 13;  Length 128;
  Best Local Similarity   54.4%;  Pred. No. 1.9e-27;
  Matches   56;  Conservative   12;  Mismatches   35;  Indels    0;  Gaps    0;

Qy          3 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 62
Db         25 DWETFQKKHLTDTKKVKCDVEMAKALFDCKKTNTFIYALPGRVKALCKNIRDNTDVLSRD 84

Qy         63 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
Db         85 AFLLPQCDRIKLPCHYKLSSSTNTICITCVNQLPIHFAGVGSC 127


RESULT 6
Q9DFY5
ID   Q9DFY5      PRELIMINARY;      PRT;   128 AA.
AC   Q9DFY5;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RC-RNase6 ribonuclease precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20512555; PubMed=11058105;
RA   Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT   "Purification and cloning of cytotoxic ribonucleases from Rana
RT   catesbeiana (bullfrog).";
RL   Nucleic Acids Res. 28:4097-4104(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF242556; AAG31442.2; -.
DR   HSSP; P22069; 1ONC.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL       1     23       POTENTIAL.
FT   CHAIN       24    128       RC-RNASE6 RIBONUCLEASE.
SQ   SEQUENCE   128 AA;  14804 MW;  AFEBFD67D266C7C2 CRC64;

  Query Match             52.2%;  Score 304;  DB 13;  Length 128;
  Best Local Similarity   53.4%;  Pred. No. 3.2e-27;
  Matches   55;  Conservative   13;  Mismatches   35;  Indels    0;  Gaps    0;

Qy          3 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 62
Db         25 DWDTFQKKHLTDTKKVKCDVEMKKALFDCKKTNTFIFARPPRVQALCKNIKDNTNVLSRD 84

Qy         63 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
Db         85 VFYLPQCNRKKLPCHYRLDGSTNTICLTCMKELPIHFAGVGKC 127


RESULT 7
Q98SM0
ID   Q98SM0      PRELIMINARY;      PRT;   133 AA.
AC   Q98SM0;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RNase A-type ribonuclease rc208 precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21539506; PubMed=11683320;
RA   Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT   "Rapid diversification of RNase A superfamily ribonuclease from the
RT   bullfrog, Rana catesbeiana.";
RL   J. Mol. Evol. 53:31-38(2001).
DR   EMBL; AF351209; AAK30255.1; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNase_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL       1     22       POTENTIAL.
SQ   SEQUENCE   133 AA;  14628 MW;  87FCF122C3499E02 CRC64;

  Query Match             50.3%;  Score 293;  DB 13;  Length 133;
  Best Local Similarity   49.1%;  Pred. No. 6.1e-26;
  Matches   54;  Conservative   16;  Mismatches   32;  Indels    8;  Gaps    3;

Qy          3 DWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV 58
Db         24 NWATFQQKHITNTSSINCNTIMDNNIYIVGGQCKGVNTFIISSATTVKAICTGVI-NMNV 82

Qy         59 LTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         25 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 84

Qy         63 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
              |||||||||||||||||||||||||||||||||||||||||||
Db         85 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 127


RESULT 2
Q8UVX5
ID   Q8UVX5      PRELIMINARY;      PRT;   127 AA.
AC   Q8UVX5;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Onconase precursor.
GN   RPR.
OS   Rana pipiens (Northern leopard frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8404;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Liao Y.-D., Wang S.-C.;
RT   "Rana pipiens onconase genomic DNA.";
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF332139; AAL54383.1; -.
DR   PIR; A39035; A39035.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     23       POTENTIAL.
SQ   SEQUENCE   127 AA;  14469 MW;  953F90D351CFEEF3 CRC64;

  Query Match             94.7%;  Score 551;  DB 13;  Length 127;
  Best Local Similarity   96.1%;  Pred. No. 1e-55;
  Matches   99;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 62
              |||||||||:|||||||:||||||||||||||||||||||||||||||||||||||||||
Db         25 DWLTFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 84

Qy         63 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
              |||||||||||||||||||| |||||||||||||||| |
Db         85 EFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 127


RESULT 3
Q9DFY6
ID   Q9DFY6      PRELIMINARY;      PRT;   129 AA.
AC   Q9DFY6;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RC-RNase4 ribonuclease precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20512555; PubMed=11058105;
RA   Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT   "Purification and cloning of cytotoxic ribonucleases from Rana
RT   catesbeiana (bullfrog).";
RL   Nucleic Acids Res. 28:4097-4104(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF242555; AAG31441.2; -.
DR   PDB; 1KVZ; 28-JUL-02.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24    129       RC-RNASE4 RIBONUCLEASE.
SQ   SEQUENCE   129 AA;  14724 MW;  826A62882B10ABDA CRC64;

  Query Match             68.6%;  Score 399.5;  DB 13;  Length 129;
  Best Local Similarity   67.3%;  Pred. No. 3.1e-38;
  Matches   70;  Conservative   16;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          3 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 62
              || ||:|||||:| ||||:|:|  |:|| |||||||||| | ||||:|:|:| | :||: |
Db         25 DWATFKKKHLTDTWDVDCDNLMPTSLFDCKDKNTFIYSLPGPVKALCRGVIFSADVLSNS 84

Qy         63 EFYLSDCNVTSR-PCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
              ||||::|||  | |||||||||:|  |: ||:: |||| ||| |
Db         85 EFYLAECNVKPRKPCKYKLKKSSNRICIRCEHELPVHFAGVGIC 128


RESULT 4
Q9DFY8
ID   Q9DFY8      PRELIMINARY;      PRT;   128 AA.
AC   Q9DFY8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RC-RNase2 ribonuclease precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20512555; PubMed=11058105;
RA   Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT   "Purification and cloning of cytotoxic ribonucleases from Rana
RT   catesbeiana (bullfrog).";
RL   Nucleic Acids Res. 28:4097-4104(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF242553; AAG31439.1; -.
DR   PDB; 1M58; 09-JAN-03.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24    128       RC-RNASE2 RIBONUCLEASE.
SQ   SEQUENCE   128 AA;  14839 MW;  989719CF52053ECC CRC64;

  Query Match             65.5%;  Score 381;  DB 13;  Length 128;
  Best Local Similarity   67.0%;  Pred. No. 4.2e-36;
  Matches   69;  Conservative   10;  Mismatches   24;  Indels    0;  Gaps    0;

Qy          3 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 62
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:10 ; Search time 29.8597 Seconds
(without alignments)
1109.503 Million cell updates/sec

Title: US-09-961-400-13
Perfect score: 582
Sequence: 1 MSDWLTFQKKHLTNTRDVDC.....TFCVTCENQAPVHFVGVGHC 105

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	573	98.5	127	13	Q9I8V8	Q9i8v8 rana pipien
2	551	94.7	127	13	Q8UVX5	Q8uvx5 rana pipien
3	399.5	68.6	129	13	Q9DFY6	Q9dfy6 rana catesb
4	381	65.5	128	13	Q9DFY8	Q9dfy8 rana catesb
5	306	52.6	128	13	Q9DFY7	Q9dfy7 rana catesb
6	304	52.2	128	13	Q9DFY5	Q9dfy5 rana catesb
7	293	50.3	133	13	Q98SM0	Q98sm0 rana catesb
8	281	48.3	132	13	Q98SM2	Q98sm2 rana catesb
9	281	48.3	133	13	Q98SL9	Q98sl9 rana catesb
10	277	47.6	133	13	Q98SL8	Q98sl8 rana catesb
11	275	47.3	132	13	Q98SM1	Q98sm1 rana catesb
12	270.5	46.5	132	13	Q9DF78	Q9df78 rana catesb
13	157.5	27.1	169	13	Q9W738	Q9w738 xenopus lae
14	133	22.9	152	11	Q9JKI5	Q9jki5 mus saxicol
15	131	22.5	157	11	Q9JKI9	Q9jki9 meriones un
16	130.5	22.4	153	11	Q9JKI7	Q9jki7 mus saxicol
17	130	22.3	157	11	Q9JKJ3	Q9jkj3 meriones un
18	128.5	22.1	146	6	Q861Y3	Q861y3 pygathrix r
19	128.5	22.1	146	6	Q861Y2	Q861y2 pygathrix b
20	128.5	22.1	146	6	Q861Y1	Q861y1 pygathrix a
21	127	21.8	154	11	Q9JKI8	Q9jki8 mus saxicol
22	127	21.8	157	11	Q9JKJ4	Q9jkj4 meriones un
23	126	21.6	157	11	Q9JKJ1	Q9jkj1 meriones un
24	125	21.5	157	11	Q9JKJ2	Q9jkj2 meriones un
25	124.5	21.4	146	6	Q861Y4	Q861y4 trachypithe
26	124.5	21.4	155	11	Q9JKH9	Q9jkh9 mus pahari
27	123.5	21.2	155	11	Q9JKI3	Q9jki3 mus saxicol
28	121	20.8	147	6	Q7YRJ6	Q7yrj6 balaena mys
29	120.5	20.7	155	11	Q9JKI6	Q9jki6 mus saxicol
30	119.5	20.5	155	11	Q9JKI2	Q9jki2 mus saxicol
31	119.5	20.5	155	11	Q9JKI4	Q9jki4 mus saxicol
32	118	20.3	147	6	Q7YRJ5	Q7yrj5 tursiops tr
33	117.5	20.2	155	11	Q9R134	Q9r134 rattus norv
34	117	20.1	156	11	Q9JKG6	Q9jkg6 mus caroli
35	117	20.1	156	11	Q9JKH7	Q9jkh7 mus caroli
36	116.5	20.0	132	6	Q9TV25	Q9tv25 eulemur ful
37	116.5	20.0	132	6	Q9TV24	Q9tv24 galago moho
38	116.5	20.0	155	11	Q9R125	Q9r125 mus musculu
39	116.5	20.0	155	11	Q9JKH8	Q9jkh8 mus pahari
40	116	19.9	156	11	Q9JKG7	Q9jkg7 mus caroli
41	115	19.8	146	6	Q861Y5	Q861y5 colobus gue
42	115	19.8	156	11	Q9JKH4	Q9jkh4 mus caroli
43	115	19.8	156	11	Q9JKG9	Q9jkg9 mus caroli
44	115	19.8	156	11	Q9JKH5	Q9jkh5 mus caroli
45	114.5	19.7	170	6	Q9BEC1	Q9bec1 tragulus ja

ALIGNMENTS

RESULT 1
Q9I8V8
ID Q9I8V8 PRELIMINARY; PRT; 127 AA.
AC Q9I8V8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Onconase variant rapLR1 precursor.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20330357; PubMed=10871370;
RA Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;
RT "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a
RT 3' UTR of unusual length and structure.";
RL Nucleic Acids Res. 28:2375-2382(2000).
DR EMBL; AF165133; AAF76935.1; -.
DR PIR; A39035; A39035.
DR HSSP; P22069; 1ONC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNAse_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
SQ SEQUENCE 127 AA; 14491 MW; B8511DC5407AB69B CRC64;

Query Match 98.5%; Score 573; DB 13; Length 127;
Best Local Similarity 100.0%; Pred. No. 3e-58;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 62

```
Q9JKI5
ID   Q9JKI5      PRELIMINARY;      PRT;   152 AA.
AC   Q9JKI5;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Eosinophil-associated ribonuclease 10.
GN   EAR10.
OS   Mus saxicola (Spiny mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10094;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20243759; PubMed=10758160;
RA   Zhang J., Dyer K.D., Rosenberg H.F.;
RT   "Evolution of the rodent eosinophil-associated ribonuclease gene
RT   family by rapid gene sorting and positive selection.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:4701-4706(2000).
DR   EMBL; AF238398; AAF67698.1; -.
DR   HSSP; P10153; 1HI2.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
SQ   SEQUENCE   152 AA;  16830 MW;  780421C3661732C8 CRC64;

  Query Match             23.1%;  Score 133;  DB 11;  Length 152;
  Best Local Similarity   30.3%;  Pred. No. 1.8e-07;
  Matches   37;  Conservative   19;  Mismatches   42;  Indels   24;  Gaps    6;

Qy          1 SDWLTFQKKHLTNTRDVDCNNIM---STNLFHCKDKNTFIYSRPEPVKAIC---KGIIA- 53
              | |  |  :|:||| :  ||  |   : |   ||: |||:::    | :|    |: :
Db         31 SQW--FATQHITNTANPQCNVEMLPINRNRTRCKNINTFLHTHFANVVGVCGNPSGLCSN 88

Qy         54 --SKNVLTTSEFYLSDCNVTSR-----PCKYKLKKSTNTFCVTCENQAP--------VHF 98
                | |   :|   :: ||:|||      |:|: | |   : | |  : |         ||
Db         89 NISTNCHNSSRVPITVCNITSREKSCTQCRYQTKGSVEYYTVACNPRTPQDSPRYPVVHL 148

Qy         99 VG 100
              |
Db        149 DG 150


RESULT 15
Q9JKI9
ID   Q9JKI9      PRELIMINARY;      PRT;   157 AA.
AC   Q9JKI9;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Eosinophil-associated ribonuclease 44.
GN   EAR44.
OS   Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC   Meriones.
OX   NCBI_TaxID=10047;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20243759; PubMed=10758160;
RA   Zhang J., Dyer K.D., Rosenberg H.F.;
RT   "Evolution of the rodent eosinophil-associated ribonuclease gene
RT   family by rapid gene sorting and positive selection.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:4701-4706(2000).
DR   EMBL; AF238394; AAF67694.1; -.
DR   HSSP; P10153; 1HI2.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
SQ   SEQUENCE   157 AA;  17887 MW;  34FE2AE777EF3709 CRC64;

  Query Match             22.7%;  Score 131;  DB 11;  Length 157;
  Best Local Similarity   30.6%;  Pred. No. 3.2e-07;
  Matches   34;  Conservative   20;  Mismatches   37;  Indels   20;  Gaps    7;

Qy          1 SDWLTFQKKHLTNTRDVDCNNIM-STNLF--HCKDKNTFIYSRPEPV-------KAICKG 50
              | | | |  |::||  : ||  |   | :   ||| |||:::|   |          ||
Db         34 SQWFTIQ--HISNTTTIQCNAAMLGVNNYTGRCKDLNTFLHTRFANVVNECYNRNTTCKN 91

Qy         51 IIASKNVL-TTSEFYLSDCNVTS-----RPCKYKLKKSTNTFCVTCENQAP 95
                :|   : |:  ::|||:||      | |:|:  ::   : : | |: |
Db         92 --GRRNCHDSRSKVSITDCNLTSPSANYRQCRYQRTRARKFYRIACNNKTP 140


Search completed: May  7, 2004, 21:46:02
Job time : 29.5753 secs
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RESULT 11
Q98SM1
ID   Q98SM1      PRELIMINARY;      PRT;   132 AA.
AC   Q98SM1;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RNase A-type ribonuclease rc204 precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21539506; PubMed=11683320;
RA   Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT   "Rapid diversification of RNase A superfamily ribonuclease from the
RT   bullfrog, Rana catesbeiana.";
RL   J. Mol. Evol. 53:31-38(2001).
DR   EMBL; AF351208; AAK30254.1; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     22       POTENTIAL.
SQ   SEQUENCE   132 AA;  14704 MW;  95D61760F729868E CRC64;

  Query Match             47.7%;  Score 275;  DB 13;  Length 132;
  Best Local Similarity   48.2%;  Pred. No. 6e-24;
  Matches   53;  Conservative   14;  Mismatches   35;  Indels    8;  Gaps    3;

Qy          2 DWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV 57
              || |||:||: :|  :||| ||  :::     ||  ||||      |||||  |:: | ||
Db         24 DWPTFQQKHIPSTSSIDCNTIMDKDIYIVRGQCKKVNTFIIYSATTVKAICTGVLNS-NV 82

Qy         58 LTTSEFYLSDCN---VTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
              |:|: | |       :|||| |   | ||  || |||: |||| |:| |
Db         83 LSTTRFQLXXXTRTFITSRPCPYSSTKETNKICVKCENEYPVHFAGIGKC 132


RESULT 12
Q9DF78
ID   Q9DF78      PRELIMINARY;      PRT;   132 AA.
AC   Q9DF78;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RC-RNaseL1 ribonuclease precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20512555; PubMed=11058105;
RA   Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT   "Purification and cloning of cytotoxic ribonucleases from Rana
RT   catesbeiana (bullfrog).";
RL   Nucleic Acids Res. 28:4097-4104(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF288642; AAG30414.2; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    132       RC-RNASEL1 RIBONUCLEASE.
SQ   SEQUENCE   132 AA;  14625 MW;  D8D9A517452FBE53 CRC64;

  Query Match             46.9%;  Score 270.5;  DB 13;  Length 132;
  Best Local Similarity   43.6%;  Pred. No. 2e-23;
  Matches   48;  Conservative   19;  Mismatches   36;  Indels    7;  Gaps    2;

Qy          2 DWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV 57
              :|  |::||:|:|  :||| ||   ::     ||::|||| |  : ||||| |:   :
Db         23 NWAKFKEKHITSTSSIDCNTIMDKAIYIVGGKCKERNTFIISSEDNVKAICSGVSPDRKE 82

Qy         58 LTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
              |:|: | |: |   ::| ||| |      |  || || | ||||||:| |
Db         83 LSTTSFKLNTCIRDSITPRPCPYHPSPDNNKICVKCEKQLPVHFVGIGKC 132


RESULT 13
Q9W738
ID   Q9W738      PRELIMINARY;      PRT;   169 AA.
AC   Q9W738;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   FRL2 protein.
GN   FRL2.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96069863; PubMed=7585965;
RA   Kinoshita N., Minshull J., Kirschner M.W.;
RT   "The identification of two novel ligands of the FGF receptor by a
RT   yeast screening method and their activity in Xenopus development.";
RL   Cell 83:621-630(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Kinoshita N., Kirschner M.W.;
RL   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF159166; AAD41901.1; -.
DR   HSSP; P00656; 1LSQ.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
SQ   SEQUENCE   169 AA;  18891 MW;  D969F3E43B3CE1B8 CRC64;

  Query Match             27.3%;  Score 157.5;  DB 13;  Length 169;
  Best Local Similarity   36.1%;  Pred. No. 3e-10;
  Matches   39;  Conservative   19;  Mismatches   35;  Indels   15;  Gaps    6;

Qy          6 FQKKHLTNT-RDVDCN------NIMSTNLFHCKDKNTFIY-SRPEPVKAICKGIIASKNV 57
              | :||:     : :||       ||    |  :|| :|||: :  : || :| ||: |  |
Db         33 FMEKHIVKEGAETNCNQTIKDRNIRFKN--NCKFRNTFIHDTNGKKVKEMCAGIVKSTFV 90

Qy         58 LTTSEFYLSDCNV---TSRP--CKYKLKKSTNTFCVTCENQAPVHFVG 100
              ::     |:|| :   |:||  | |   ::|    :|||  |||| |
Db         91 ISKELLPLTDCLLMGRTARPPNCAYNQTRTTGVINITCENNYPVHFAG 138


RESULT 14
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                  |:|: | |: |   ::| ||| |  :   |  || |||| |||| |:| |
Db          83 LSTTRFQLNTCTRTSITPRPCPYSSRTENNYICVKCENQYPVHFAGIGRC 132


RESULT 8
Q98SM2
ID   Q98SM2      PRELIMINARY;      PRT;   132 AA.
AC   Q98SM2;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21539506; PubMed=11683320;
RA   Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT   "Rapid diversification of RNase A superfamily ribonuclease from the
RT   bullfrog, Rana catesbeiana.";
RL   J. Mol. Evol. 53:31-38(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Tang P.-C., Jeng J.-T.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF351207; AAK30253.1; -.
DR   EMBL; AF359578; AAL87036.1; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     22       POTENTIAL.
FT   CHAIN        23    132       RC-RNASE7.
SQ   SEQUENCE   132 AA;  14412 MW;  131A745187978687 CRC64;

  Query Match             48.7%;  Score 281;  DB 13;  Length 132;
  Best Local Similarity   47.7%;  Pred. No. 1.2e-24;
  Matches   52;  Conservative   14;  Mismatches   35;  Indels    8;  Gaps    3;

Qy           3 WLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNVL 58
               |  ||:||: :|  ::|| ||  |::     ||  |||| |    |||||  | : : |||
Db          25 WAKFQQKHIPSTSSINCNTIMDNNIYIVGGQCKKVNTFIISSATTVKAICNG-VTNSNVL 83

Qy          59 TTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
               : : | |  |   ::| ||| |  || ||  || |||| |||| |:| |
Db          84 SPTRFQLDTCTRTSITPRPCPYSSKKETNKICVKCENQLPVHFAGIGKC 132


RESULT 9
Q98SL9
ID   Q98SL9      PRELIMINARY;      PRT;   133 AA.
AC   Q98SL9;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RNase A-type ribonuclease rc212 precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21539506; PubMed=11683320;
RA   Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT   "Rapid diversification of RNase A superfamily ribonuclease from the
RT   bullfrog, Rana catesbeiana.";
RL   J. Mol. Evol. 53:31-38(2001).
DR   EMBL; AF351210; AAK30256.1; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     22       POTENTIAL.
SQ   SEQUENCE   133 AA;  14615 MW;  C8785B236B26E54E CRC64;

  Query Match             48.7%;  Score 281;  DB 13;  Length 133;
  Best Local Similarity   47.3%;  Pred. No. 1.2e-24;
  Matches   52;  Conservative   17;  Mismatches   33;  Indels    8;  Gaps    3;

Qy           2 DWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV 57
               :| |||:||:|||  ::|:|||: :|:     ||  |||| |    || || | :  | |
Db          24 NWATFQQKHITNTSSINCSNIMNNSLYIVGGQCKKVNTFIASSATTVKGICSG-VTDKKV 82

Qy          58 LTTSEFYLSDCN---VTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
               |::::| | |    :| ||| |  :  ||  || |||| |||| |:| |
Db          83 LSSTKFQLDICTRIFITPRPCPYSSRTETNYICVKCENQYPVHFAGIGQC 132


RESULT 10
Q98SL8
ID   Q98SL8      PRELIMINARY;      PRT;   133 AA.
AC   Q98SL8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RNase A-type ribonuclease rc218 precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21539506; PubMed=11683320;
RA   Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT   "Rapid diversification of RNase A superfamily ribonuclease from the
RT   bullfrog, Rana catesbeiana.";
RL   J. Mol. Evol. 53:31-38(2001).
DR   EMBL; AF351211; AAK30257.1; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     22       POTENTIAL.
SQ   SEQUENCE   133 AA;  14590 MW;  8B40B9A94FA5B943 CRC64;

  Query Match             48.0%;  Score 277;  DB 13;  Length 133;
  Best Local Similarity   46.4%;  Pred. No. 3.6e-24;
  Matches   51;  Conservative   18;  Mismatches   33;  Indels    8;  Gaps    3;

Qy           2 DWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV 57
               :| |||::|:|||  ::|:|||: :|:     ||  |||| |    || || | :  | |
Db          24 NWATFQEQHITNTSSINCSNIMNNSLYIVGGQCKKVNTFIASSATTVKGICSG-VTDKKV 82

Qy          58 LTTSEFYLSDCN---VTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
               |::::| | |    :| ||| |  :  ||  || |||| |||| |:| |
Db          83 LSSTKFQLDICTRIFITPRPCPYSSRTETNYICVKCENQYPVHFAGIGQC 132
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Db         25 NWETFQKKHLTDTRDVKCDAEMKKALFDCKQKNTFIYARPGRVQALCKNIIVSKNVLSTD 84

Qy         62 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
              ||||||||    || ||||||:|| |:||||: ||||| |  |
Db         85 EFYLSDCNRIKLPCHYKLKKSSNTICITCENKLPVHFVAVEEC 127


RESULT 5
Q9DFY7
ID   Q9DFY7      PRELIMINARY;      PRT;   128 AA.
AC   Q9DFY7;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RC-RNase3 ribonuclease precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20512555; PubMed=11058105;
RA   Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT   "Purification and cloning of cytotoxic ribonucleases from Rana
RT   catesbeiana (bullfrog).";
RL   Nucleic Acids Res. 28:4097-4104(2000).
DR   EMBL; AF242554; AAG31440.2; -.
DR   HSSP; P22069; 1ONC.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24    128       RC-RNASE3 RIBONUCLEASE.
SQ   SEQUENCE   128 AA;  14517 MW;  2B14986082E0587D CRC64;

  Query Match             53.0%;  Score 306;  DB 13;  Length 128;
  Best Local Similarity   54.4%;  Pred. No. 1.5e-27;
  Matches   56;  Conservative   12;  Mismatches   35;  Indels    0;  Gaps    0;

Qy          2 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 61
              || |||||||:|: | |:  |:  || ||  |||||: |  |||:|| |  : :||:
Db         25 DWETFQKKHLTDTKKVKCDVEMAKALFDCKKTNTFIYALPGRVKALCKNIRDNTDVLSRD 84

Qy         62 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
               | |  |:    || |||  |||| |:|| || |:|| ||| |
Db         85 AFLLPQCDRIKLPCHYKLSSSTNTICITCVNQLPIHFAGVGSC 127


RESULT 6
Q9DFY5
ID   Q9DFY5      PRELIMINARY;      PRT;   128 AA.
AC   Q9DFY5;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RC-RNase6 ribonuclease precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20512555; PubMed=11058105;
RA   Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT   "Purification and cloning of cytotoxic ribonucleases from Rana
RT   catesbeiana (bullfrog).";
RL   Nucleic Acids Res. 28:4097-4104(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF242556; AAG31442.2; -.
DR   HSSP; P22069; 1ONC.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24    128       RC-RNASE6 RIBONUCLEASE.
SQ   SEQUENCE   128 AA;  14804 MW;  AFEBFD67D266C7C2 CRC64;

  Query Match             52.7%;  Score 304;  DB 13;  Length 128;
  Best Local Similarity   53.4%;  Pred. No. 2.6e-27;
  Matches   55;  Conservative   13;  Mismatches   35;  Indels    0;  Gaps    0;

Qy          2 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 61
              || |||||||:|: | |:  |   || ||  ||||::||  |:|:|| |  : |||:
Db         25 DWDTFQKKHLTDTKKVKCDVEMKKALFDCKKTNTFIFARPPRVQALCKNIKDNTNVLSRD 84

Qy         62 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
               |||  ||    || |:|  |||| |:||  : |:|| ||| |
Db         85 VFYLPQCNRKKLPCHYRLDGSTNTICLTCMKELPIHFAGVGKC 127


RESULT 7
Q98SM0
ID   Q98SM0      PRELIMINARY;      PRT;   133 AA.
AC   Q98SM0;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RNase A-type ribonuclease rc208 precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21539506; PubMed=11683320;
RA   Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT   "Rapid diversification of RNase A superfamily ribonuclease from the
RT   bullfrog, Rana catesbeiana.";
RL   J. Mol. Evol. 53:31-38(2001).
DR   EMBL; AF351209; AAK30255.1; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     22       POTENTIAL.
SQ   SEQUENCE   133 AA;  14628 MW;  87FCF122C3499E02 CRC64;

  Query Match             50.8%;  Score 293;  DB 13;  Length 133;
  Best Local Similarity   49.1%;  Pred. No. 5e-26;
  Matches   54;  Conservative   16;  Mismatches   32;  Indels    8;  Gaps    3;

Qy          2 DWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV 57
              :| |||:||:|||  ::|| ||  |::     ||  |||| |    |||| |:| : ||
Db         24 NWATFQQKHITNTSSINCNTIMDNNIYIVGGQCKGVNTFIISSATTVKAICTGVI-NMNV 82

Qy         58 LTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          25 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 84

Qy          62 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
               |||||||||||||||||||||||||||||||||||||||||||
Db          85 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 127


RESULT 2
Q8UVX5
ID   Q8UVX5      PRELIMINARY;      PRT;   127 AA.
AC   Q8UVX5;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Onconase precursor.
GN   RPR.
OS   Rana pipiens (Northern leopard frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8404;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Liao Y.-D., Wang S.-C.;
RT   "Rana pipiens onconase genomic DNA.";
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF332139; AAL54383.1; -.
DR   PIR; A39035; A39035.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     23       POTENTIAL.
SQ   SEQUENCE   127 AA;  14469 MW;  953F90D351CFEEF3 CRC64;

  Query Match             95.5%;  Score 551;  DB 13;  Length 127;
  Best Local Similarity   96.1%;  Pred. No. 7.1e-56;
  Matches   99;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy           2 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 61
               |||||||||:|||||||:|||||||||||||||||||||||||||||||||||||||||||
Db          25 DWLTFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 84

Qy          62 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
               |||||||||||||||||||||| |||||||||||||||| |
Db          85 EFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 127


RESULT 3
Q9DFY6
ID   Q9DFY6      PRELIMINARY;      PRT;   129 AA.
AC   Q9DFY6;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RC-RNase4 ribonuclease precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20512555; PubMed=11058105;
RA   Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT   "Purification and cloning of cytotoxic ribonucleases from Rana
RT   catesbeiana (bullfrog).";
RL   Nucleic Acids Res. 28:4097-4104(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF242555; AAG31441.2; -.
DR   PDB; 1KVZ; 28-JUL-02.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24    129       RC-RNASE4 RIBONUCLEASE.
SQ   SEQUENCE   129 AA;  14724 MW;  826A62882B10ABDA CRC64;

  Query Match             69.2%;  Score 399.5;  DB 13;  Length 129;
  Best Local Similarity   67.3%;  Pred. No. 2.4e-38;
  Matches   70;  Conservative   16;  Mismatches   17;  Indels    1;  Gaps    1;

Qy           2 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 61
               || ||:|||||:| ||||:|:| |:|| |||||||||| | ||||:|:|:|:| | :||: |
Db          25 DWATFKKKHLTDTWDVDCDNLMPTSLFDCKDKNTFIYSLPGPVKALCRGVIFSADVLSNS 84

Qy          62 EFYLSDCNVTSR-PCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
               ||||::|||  | |||||||||:|  |: ||:: |||| ||| |
Db          85 EFYLAECNVKPRKPCKYKLKKSSNRICIRCEHELPVHFAGVGIC 128


RESULT 4
Q9DFY8
ID   Q9DFY8      PRELIMINARY;      PRT;   128 AA.
AC   Q9DFY8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RC-RNase2 ribonuclease precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20512555; PubMed=11058105;
RA   Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT   "Purification and cloning of cytotoxic ribonucleases from Rana
RT   catesbeiana (bullfrog).";
RL   Nucleic Acids Res. 28:4097-4104(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF242553; AAG31439.1; -.
DR   PDB; 1M58; 09-JAN-03.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24    128       RC-RNASE2 RIBONUCLEASE.
SQ   SEQUENCE   128 AA;  14839 MW;  989719CF52053ECC CRC64;

  Query Match             66.0%;  Score 381;  DB 13;  Length 128;
  Best Local Similarity   67.0%;  Pred. No. 3.2e-36;
  Matches   69;  Conservative   10;  Mismatches   24;  Indels    0;  Gaps    0;

Qy           2 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 61
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:10 ; Search time 29.5753 Seconds
(without alignments)
1109.503 Million cell updates/sec

Title: US-09-961-400-11
Perfect score: 577
Sequence: 1 SDWLTFQKKHLTNTRDVDCN.....TFCVTCENQAPVHFVGVGHC 104

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	573	99.3	127	13	Q9I8V8	Q9i8v8 rana pipien
2	551	95.5	127	13	Q8UVX5	Q8uvx5 rana pipien
3	399.5	69.2	129	13	Q9DFY6	Q9dfy6 rana catesb
4	381	66.0	128	13	Q9DFY8	Q9dfy8 rana catesb
5	306	53.0	128	13	Q9DFY7	Q9dfy7 rana catesb
6	304	52.7	128	13	Q9DFY5	Q9dfy5 rana catesb
7	293	50.8	133	13	Q98SM0	Q98sm0 rana catesb
8	281	48.7	132	13	Q98SM2	Q98sm2 rana catesb
9	281	48.7	133	13	Q98SL9	Q98sl9 rana catesb
10	277	48.0	133	13	Q98SL8	Q98sl8 rana catesb
11	275	47.7	132	13	Q98SM1	Q98sm1 rana catesb
12	270.5	46.9	132	13	Q9DF78	Q9df78 rana catesb
13	157.5	27.3	169	13	Q9W738	Q9w738 xenopus lae
14	133	23.1	152	11	Q9JKI5	Q9jki5 mus saxicol
15	131	22.7	157	11	Q9JKI9	Q9jki9 meriones un
16	130.5	22.6	153	11	Q9JKI7	Q9jki7 mus saxicol
17	130	22.5	157	11	Q9JKJ3	Q9jkj3 meriones un
18	128.5	22.3	146	6	Q861Y3	Q861y3 pygathrix r
19	128.5	22.3	146	6	Q861Y2	Q861y2 pygathrix b
20	128.5	22.3	146	6	Q861Y1	Q861y1 pygathrix a
21	127	22.0	154	11	Q9JKI8	Q9jki8 mus saxicol
22	127	22.0	157	11	Q9JKJ4	Q9jkj4 meriones un
23	126	21.8	157	11	Q9JKJ1	Q9jkj1 meriones un
24	125	21.7	157	11	Q9JKJ2	Q9jkj2 meriones un
25	124.5	21.6	146	6	Q861Y4	Q861y4 trachypithe
26	124.5	21.6	155	11	Q9JKH9	Q9jkh9 mus pahari
27	123.5	21.4	155	11	Q9JKI3	Q9jki3 mus saxicol
28	121	21.0	147	6	Q7YRJ6	Q7yrj6 balaena mys
29	120.5	20.9	155	11	Q9JKI6	Q9jki6 mus saxicol
30	119.5	20.7	155	11	Q9JKI2	Q9jki2 mus saxicol
31	119.5	20.7	155	11	Q9JKI4	Q9jki4 mus saxicol
32	118	20.5	147	6	Q7YRJ5	Q7yrj5 tursiops tr
33	117.5	20.4	155	11	Q9R134	Q9r134 rattus norv
34	117	20.3	156	11	Q9JKG6	Q9jkg6 mus caroli
35	117	20.3	156	11	Q9JKH7	Q9jkh7 mus caroli
36	116.5	20.2	132	6	Q9TV25	Q9tv25 eulemur ful
37	116.5	20.2	155	11	Q9R125	Q9r125 mus musculu
38	116.5	20.2	155	11	Q9JKH8	Q9jkh8 mus pahari
39	116	20.1	156	11	Q9JKG7	Q9jkg7 mus caroli
40	115	19.9	146	6	Q861Y5	Q861y5 colobus gue
41	115	19.9	156	11	Q9JKH4	Q9jkh4 mus caroli
42	115	19.9	156	11	Q9JKG9	Q9jkg9 mus caroli
43	115	19.9	156	11	Q9JKH5	Q9jkh5 mus caroli
44	114.5	19.8	132	6	Q9TV24	Q9tv24 galago moho
45	114.5	19.8	170	6	Q9BEC1	Q9bec1 tragulus ja

ALIGNMENTS

RESULT 1
Q9I8V8
ID Q9I8V8 PRELIMINARY; PRT; 127 AA.
AC Q9I8V8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Onconase variant rapLR1 precursor.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20330357; PubMed=10871370;
RA Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;
RT "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a
RT 3' UTR of unusual length and structure.";
RL Nucleic Acids Res. 28:2375-2382(2000).
DR EMBL; AF165133; AAF76935.1; -.
DR PIR; A39035; A39035.
DR HSSP; P22069; 1ONC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNAse_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
SQ SEQUENCE 127 AA; 14491 MW; B8511DC5407AB69B CRC64;

Query Match 99.3%; Score 573; DB 13; Length 127;
Best Local Similarity 100.0%; Pred. No. 2e-58;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 61

```
Q9JKJ3
ID   Q9JKJ3       PRELIMINARY;      PRT;   157 AA.
AC   Q9JKJ3;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Eosinophil-associated ribonuclease 25.
GN   EAR25.
OS   Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC   Meriones.
OX   NCBI_TaxID=10047;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20243759; PubMed=10758160;
RA   Zhang J., Dyer K.D., Rosenberg H.F.;
RT   "Evolution of the rodent eosinophil-associated ribonuclease gene
RT   family by rapid gene sorting and positive selection.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:4701-4706(2000).
DR   EMBL; AF238390; AAF67690.1; -.
DR   HSSP; P10153; 1HI2.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
SQ   SEQUENCE   157 AA;  17945 MW;  FDFE22FE77FE371A CRC64;

  Query Match             20.5%;  Score 120;  DB 11;  Length 157;
  Best Local Similarity   29.2%;  Pred. No. 5.4e-06;
  Matches   33;  Conservative   18;  Mismatches   34;  Indels   28;  Gaps    6;

Qy          4 WLTFQKKHLTNTRDVDCN-NILSTNLF--HCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
              | | |  |::||  : ||  :|  | :   ||| |||:::|   |   |        | |
Db         36 WFTIQ--HISNTTTIQCNAAMLGVNNYTGRCKDLNTFLHTRFANVVNEC------YNRNT 87

Qy         61 TFE-----------FYLSDCNATS-----RPCKYKLKKSTNTFCVTCENQAP 96
              | :              ::||| ||     | |:|:  ::   : : | |: |
Db         88 TCKNGRRNCHDSRSRVSITDCNLTSPSTNYRQCRYQRTRARKFYRIACNNKTP 140


RESULT 15
Q9JKI9
ID   Q9JKI9       PRELIMINARY;      PRT;   157 AA.
AC   Q9JKI9;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Eosinophil-associated ribonuclease 44.
GN   EAR44.
OS   Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC   Meriones.
OX   NCBI_TaxID=10047;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20243759; PubMed=10758160;
RA   Zhang J., Dyer K.D., Rosenberg H.F.;
RT   "Evolution of the rodent eosinophil-associated ribonuclease gene
RT   family by rapid gene sorting and positive selection.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:4701-4706(2000).
DR   EMBL; AF238394; AAF67694.1; -.
DR   HSSP; P10153; 1HI2.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
SQ   SEQUENCE   157 AA;  17887 MW;  34FE2AE777EF3709 CRC64;

  Query Match             20.5%;  Score 120;  DB 11;  Length 157;
  Best Local Similarity   29.4%;  Pred. No. 5.4e-06;
  Matches   32;  Conservative   20;  Mismatches   37;  Indels   20;  Gaps    7;

Qy          4 WLTFQKKHLTNTRDVDCN-NILSTNLF--HCKDKNTFIYSRPEPV-------KAICKGII 53
              | | |  |::||  : ||  :|  | :   ||| |||:::|   |          ||
Db         36 WFTIQ--HISNTTTIQCNAAMLGVNNYTGRCKDLNTFLHTRFANVVNECYNRNTTCKN-- 91

Qy         54 ASKNVL-TTFEFYLSDCNATS-----RPCKYKLKKSTNTFCVTCENQAP 96
                :|   :  :  ::||| ||     | |:|:  ::   : : | |: |
Db         92 GRRNCHDSRSKVSITDCNLTSPSANYRQCRYQRTRARKFYRIACNNKTP 140


Search completed: May  7, 2004, 21:46:02
Job time : 30.8597 secs
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RESULT 11
Q98SM1
ID   Q98SM1      PRELIMINARY;      PRT;   132 AA.
AC   Q98SM1;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RNase A-type ribonuclease rc204 precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21539506; PubMed=11683320;
RA   Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT   "Rapid diversification of RNase A superfamily ribonuclease from the
RT   bullfrog, Rana catesbeiana.";
RL   J. Mol. Evol. 53:31-38(2001).
DR   EMBL; AF351208; AAK30254.1; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL       1     22       POTENTIAL.
SQ   SEQUENCE   132 AA;  14704 MW;  95D61760F729868E CRC64;

  Query Match             46.2%;  Score 270;  DB 13;  Length 132;
  Best Local Similarity   47.7%;  Pred. No. 1.7e-23;
  Matches   53;  Conservative   13;  Mismatches   37;  Indels    8;  Gaps    3;

Qy          2 QDWLTFQKKHLTNTRDVDCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 57
              ||| |||:||: :|  :||| |:  :::     ||  ||||      |||||:::| | |
Db         23 QDWPTFQQKHIPSTSSIDCNTIMDKDIYIVRGQCKKVNTFIIYSATTVKAICTGVLNS-N 81

Qy         58 VLTTFEFYLSDCN---ATSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
              ||:|  | |        |||||:|   | ||  || |||: |||| |:| |
Db         82 VLSTTRFQLXXXTRTFITSRPCPYSSTKETNKICVKCENEYPVHFAGIGKC 132


RESULT 12
Q9DF78
ID   Q9DF78      PRELIMINARY;      PRT;   132 AA.
AC   Q9DF78;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RC-RNaseL1 ribonuclease precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20512555; PubMed=11058105;
RA   Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT   "Purification and cloning of cytotoxic ribonucleases from Rana
RT   catesbeiana (bullfrog).";
RL   Nucleic Acids Res. 28:4097-4104(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF288642; AAG30414.2; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL       1     21       POTENTIAL.
FT   CHAIN       22    132       RC-RNASEL1 RIBONUCLEASE.
SQ   SEQUENCE   132 AA;  14625 MW;  D8D9A517452FBE53 CRC64;

  Query Match             45.5%;  Score 265.5;  DB 13;  Length 132;
  Best Local Similarity   43.2%;  Pred. No. 5.6e-23;
  Matches   48;  Conservative   18;  Mismatches   38;  Indels    7;  Gaps    2;

Qy          2 QDWLTFQKKHLTNTRDVDCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 57
              |:|  |::||:|:|  :||| |:   ::     ||::|||| |  : ||||| |:   :
Db         22 QNWAKFKEKHITSTSSIDCNTIMDKAIYIVGGKCKERNTFIISSEDNVKAICSGVSPDRK 81

Qy         58 VLTTFEFYLSDC---NATSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
              |:|  | |: |   : | ||| |       |  || || | ||||||:| |
Db         82 ELSTTSFKLNTCIRDSITPRPCPYHPSPDNNKICVKCEKQLPVHFVGIGKC 132


RESULT 13
Q9W738
ID   Q9W738      PRELIMINARY;      PRT;   169 AA.
AC   Q9W738;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   FRL2 protein.
GN   FRL2.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96069863; PubMed=7585965;
RA   Kinoshita N., Minshull J., Kirschner M.W.;
RT   "The identification of two novel ligands of the FGF receptor by a
RT   yeast screening method and their activity in Xenopus development.";
RL   Cell 83:621-630(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Kinoshita N., Kirschner M.W.;
RL   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF159166; AAD41901.1; -.
DR   HSSP; P00656; 1LSQ.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
SQ   SEQUENCE   169 AA;  18891 MW;  D969F3E43B3CE1B8 CRC64;

  Query Match             26.5%;  Score 154.5;  DB 13;  Length 169;
  Best Local Similarity   36.1%;  Pred. No. 5.7e-10;
  Matches   39;  Conservative   18;  Mismatches   36;  Indels   15;  Gaps    6;

Qy          7 FQKKHLTNT-RDVDCN------NILSTNLFHCKDKNTFIY-SRPEPVKAICKGIIASKNV 58
              | :||:     : :||       ||   |  :|| :||||: :  : || :| ||: |  |
Db         33 FMEKHIVKEGAETNCNQTIKDRNIRFKN--NCKFRNTFIHDTNGKKVKEMCAGIVKSTFV 90

Qy         59 LTTFEFYLSDC---NATSRP--CKYKLKKSTNTFCVTCENQAPVHFVG 101
              ::     |:||      |:||  | |   ::|     :||||  |||| |
Db         91 ISKELLPLTDCLLMGRTARPPNCAYNQTRTTGVINITCENNYPVHFAG 138


RESULT 14
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                ||:|  | |: |  ||   ||| |  :   |  || |||| |||| |:| |
Db         82 VLSTTRFQLNTCTRTSITPRPCPYSSRTENNYICVKCENQYPVHFAGIGRC 132


RESULT 8
Q98SM2
ID   Q98SM2      PRELIMINARY;      PRT;   132 AA.
AC   Q98SM2;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21539506; PubMed=11683320;
RA   Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT   "Rapid diversification of RNase A superfamily ribonuclease from the
RT   bullfrog, Rana catesbeiana.";
RL   J. Mol. Evol. 53:31-38(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Tang P.-C., Jeng J.-T.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF351207; AAK30253.1; -.
DR   EMBL; AF359578; AAL87036.1; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     22       POTENTIAL.
FT   CHAIN        23    132       RC-RNASE7.
SQ   SEQUENCE   132 AA;  14412 MW;  131A745187978687 CRC64;

  Query Match             47.8%;  Score 279;  DB 13;  Length 132;
  Best Local Similarity   47.7%;  Pred. No. 1.5e-24;
  Matches   53;  Conservative   12;  Mismatches   38;  Indels    8;  Gaps    3;

Qy          2 QDWLTFQKKHLTNTRDVDCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 57
              | |  ||:||: :|  ::|| |:  |::     ||  |||| |    ||||| | : : |
Db         23 QTWAKFQQKHIPSTSSINCNTIMDNNIYIVGGQCKKVNTFIISSATTVKAICNG-VTNSN 81

Qy         58 VLTTFEFYLSDCNATS---RPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                ||:   | |  |  ||   ||| |  || ||  || |||| |||| |:| |
Db         82 VLSPTRFQLDTCTRTSITPRPCPYSSKKETNKICVKCENQLPVHFAGIGKC 132


RESULT 9
Q98SL9
ID   Q98SL9      PRELIMINARY;      PRT;   133 AA.
AC   Q98SL9;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RNase A-type ribonuclease rc212 precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21539506; PubMed=11683320;
RA   Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT   "Rapid diversification of RNase A superfamily ribonuclease from the
RT   bullfrog, Rana catesbeiana.";
RL   J. Mol. Evol. 53:31-38(2001).
DR   EMBL; AF351210; AAK30256.1; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     22       POTENTIAL.
SQ   SEQUENCE   133 AA;  14615 MW;  C8785B236B26E54E CRC64;

  Query Match             47.3%;  Score 276;  DB 13;  Length 133;
  Best Local Similarity   46.8%;  Pred. No. 3.4e-24;
  Matches   52;  Conservative   16;  Mismatches   35;  Indels    8;  Gaps    3;

Qy          2 QDWLTFQKKHLTNTRDVDCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 57
              |:| |||:||:|||  ::|:||:: :|:     ||  |||| |    || || | :  |
Db         23 QNWATFQQKHITNTSSINCSNIMNNSLYIVGGQCKKVNTFIASSATTVKGICSG-VTDKK 81

Qy         58 VLTTFEFYLSDCN---ATSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
              ||:: :| |  |     | ||| |  :  ||  || |||| |||| |:| |
Db         82 VLSSTKFQLDICTRIFITPRPCPYSSRTETNYICVKCENQYPVHFAGIGQC 132


RESULT 10
Q98SL8
ID   Q98SL8      PRELIMINARY;      PRT;   133 AA.
AC   Q98SL8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RNase A-type ribonuclease rc218 precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21539506; PubMed=11683320;
RA   Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT   "Rapid diversification of RNase A superfamily ribonuclease from the
RT   bullfrog, Rana catesbeiana.";
RL   J. Mol. Evol. 53:31-38(2001).
DR   EMBL; AF351211; AAK30257.1; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     22       POTENTIAL.
SQ   SEQUENCE   133 AA;  14590 MW;  8B40B9A94FA5B943 CRC64;

  Query Match             46.6%;  Score 272;  DB 13;  Length 133;
  Best Local Similarity   45.9%;  Pred. No. 9.9e-24;
  Matches   51;  Conservative   17;  Mismatches   35;  Indels    8;  Gaps    3;

Qy          2 QDWLTFQKKHLTNTRDVDCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 57
              |:| |||::|:|||  ::|:||:: :|:     ||  |||| |    || || | :  |
Db         23 QNWATFQEQHITNTSSINCSNIMNNSLYIVGGQCKKVNTFIASSATTVKGICSG-VTDKK 81

Qy         58 VLTTFEFYLSDCN---ATSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
              ||:: :| |  |     | ||| |  :  ||  || |||| |||| |:| |
Db         82 VLSSTKFQLDICTRIFITPRPCPYSSRTETNYICVKCENQYPVHFAGIGQC 132
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                |:| ||||||||:|||| |:  :   || || ||||||:||  |:|:|| || |||||:|
Db          24 QNWETFQKKHLTDTRDVKCDAEMKKALFDCKQKNTFIYARPGRVQALCKNIIVSKNVLST 83

Qy          62 FEFYLSDCNATSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
               ||||||||    || ||||||:|| |:||||: ||||| |  |
Db          84 DEFYLSDCNRIKLPCHYKLKKSSNTICITCENKLPVHFVAVEEC 127


RESULT 5
Q9DFY7
ID   Q9DFY7      PRELIMINARY;      PRT;   128 AA.
AC   Q9DFY7;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RC-RNase3 ribonuclease precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20512555; PubMed=11058105;
RA   Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT   "Purification and cloning of cytotoxic ribonucleases from Rana
RT   catesbeiana (bullfrog).";
RL   Nucleic Acids Res. 28:4097-4104(2000).
DR   EMBL; AF242554; AAG31440.2; -.
DR   HSSP; P22069; 1ONC.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24    128       RC-RNASE3 RIBONUCLEASE.
SQ   SEQUENCE   128 AA;  14517 MW;  2B14986082E0587D CRC64;

  Query Match             52.6%;  Score 307;  DB 13;  Length 128;
  Best Local Similarity   53.8%;  Pred. No. 8.2e-28;
  Matches   56;  Conservative   13;  Mismatches   35;  Indels    0;  Gaps    0;

Qy           2 QDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 61
               ||| ||||||||:|: | |:  ::  || ||  |||||: |  |||:|| |  : :||:
Db          24 QDWETFQKKHLTDTKKVKCDVEMAKALFDCKKTNTFIYALPGRVKALCKNIRDNTDVLSR 83

Qy          62 FEFYLSDCNATSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                 | |  |:    || |||  |||| |:|| || |:|| ||| |
Db          84 DAFLLPQCDRIKLPCHYKLSSSTNTICITCVNQLPIHFAGVGSC 127


RESULT 6
Q9DFY5
ID   Q9DFY5      PRELIMINARY;      PRT;   128 AA.
AC   Q9DFY5;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RC-RNase6 ribonuclease precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20512555; PubMed=11058105;
RA   Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT   "Purification and cloning of cytotoxic ribonucleases from Rana
RT   catesbeiana (bullfrog).";
RL   Nucleic Acids Res. 28:4097-4104(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF242556; AAG31442.2; -.
DR   HSSP; P22069; 1ONC.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24    128       RC-RNASE6 RIBONUCLEASE.
SQ   SEQUENCE   128 AA;  14804 MW;  AFEBFD67D266C7C2 CRC64;

  Query Match             52.2%;  Score 305;  DB 13;  Length 128;
  Best Local Similarity   52.9%;  Pred. No. 1.4e-27;
  Matches   55;  Conservative   14;  Mismatches   35;  Indels    0;  Gaps    0;

Qy           2 QDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 61
               ||| ||||||||:|: | |:  :   || ||  ||||::||  |:|:|| |  : |||:
Db          24 QDWDTFQKKHLTDTKKVKCDVEMKKALFDCKKTNTFIFARPPRVQALCKNIKDNTNVLSR 83

Qy          62 FEFYLSDCNATSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                 |||  ||    || |:|  |||| |:||  : |:|| ||| |
Db          84 DVFYLPQCNRKKLPCHYRLDGSTNTICLTCMKELPIHFAGVGKC 127


RESULT 7
Q98SM0
ID   Q98SM0      PRELIMINARY;      PRT;   133 AA.
AC   Q98SM0;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RNase A-type ribonuclease rc208 precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21539506; PubMed=11683320;
RA   Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT   "Rapid diversification of RNase A superfamily ribonuclease from the
RT   bullfrog, Rana catesbeiana.";
RL   J. Mol. Evol. 53:31-38(2001).
DR   EMBL; AF351209; AAK30255.1; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     22       POTENTIAL.
SQ   SEQUENCE   133 AA;  14628 MW;  87FCF122C3499E02 CRC64;

  Query Match             50.0%;  Score 292;  DB 13;  Length 133;
  Best Local Similarity   49.5%;  Pred. No. 4.7e-26;
  Matches   55;  Conservative   14;  Mismatches   34;  Indels    8;  Gaps    3;

Qy           2 QDWLTFQKKHLTNTRDVDCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 57
               |:| |||:||:|||  ::|| |:  |::     ||  |||| |    ||||| |:| : |
Db          23 QNWATFQQKHITNTSSINCNTIMDNNIYIVGGQCKGVNTFIISSATTVKAICTGVI-NMN 81

Qy          58 VLTTFEFYLSDCNATS---RPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
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                    ||||||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||
Db          24 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 83

Qy          62 FEFYLSDCNATSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                ||||||||  |||||||||||||||||||||||||||||||||
Db          84 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 127


RESULT 2
Q8UVX5
ID   Q8UVX5      PRELIMINARY;      PRT;   127 AA.
AC   Q8UVX5;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Onconase precursor.
GN   RPR.
OS   Rana pipiens (Northern leopard frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8404;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Liao Y.-D., Wang S.-C.;
RT   "Rana pipiens onconase genomic DNA.";
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF332139; AAL54383.1; -.
DR   PIR; A39035; A39035.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     23       POTENTIAL.
SQ   SEQUENCE   127 AA;  14469 MW;  953F90D351CFEEF3 CRC64;

  Query Match             93.0%;  Score 543;  DB 13;  Length 127;
  Best Local Similarity   93.3%;  Pred. No. 3.1e-55;
  Matches   97;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy           2 QDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 61
                ||||||||||:||||||||:||:||||||||||||||||||||||||||||||||||||||
Db          24 QDWLTFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 83

Qy          62 FEFYLSDCNATSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                ||||||||  ||||||||||||||||  |||||||||||||||
Db          84 SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 127


RESULT 3
Q9DFY6
ID   Q9DFY6      PRELIMINARY;      PRT;   129 AA.
AC   Q9DFY6;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RC-RNase4 ribonuclease precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20512555; PubMed=11058105;
RA   Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT   "Purification and cloning of cytotoxic ribonucleases from Rana
RT   catesbeiana (bullfrog).";
RL   Nucleic Acids Res. 28:4097-4104(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF242555; AAG31441.2; -.
DR   PDB; 1KVZ; 28-JUL-02.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24    129       RC-RNASE4 RIBONUCLEASE.
SQ   SEQUENCE   129 AA;  14724 MW;  826A62882B10ABDA CRC64;

  Query Match             67.0%;  Score 391.5;  DB 13;  Length 129;
  Best Local Similarity   64.8%;  Pred. No. 1.3e-37;
  Matches   68;  Conservative   17;  Mismatches   19;  Indels    1;  Gaps    1;

Qy           2 QDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 61
                |||  ||:|||||:| ||||:|:: |:|| ||||||||||  | ||||:|:|:|  | :||:
Db          24 QDWATFKKKHLTDTWDVDCDNLMPTSLFDCKDKNTFIYSLPGPVKALCRGVIFSADVLSN 83

Qy          62 FEFYLSDCNATSR-PCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                ||||::||    | ||||||||||:|  |: ||::  |||| ||| |
Db          84 SEFYLAECNVKPRKPCKYKLKKSSNRICIRCEHELPVHFAGVGIC 128


RESULT 4
Q9DFY8
ID   Q9DFY8      PRELIMINARY;      PRT;   128 AA.
AC   Q9DFY8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RC-RNase2 ribonuclease precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20512555; PubMed=11058105;
RA   Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT   "Purification and cloning of cytotoxic ribonucleases from Rana
RT   catesbeiana (bullfrog).";
RL   Nucleic Acids Res. 28:4097-4104(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF242553; AAG31439.1; -.
DR   PDB; 1M58; 09-JAN-03.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24    128       RC-RNASE2 RIBONUCLEASE.
SQ   SEQUENCE   128 AA;  14839 MW;  989719CF52053ECC CRC64;

  Query Match             65.4%;  Score 382;  DB 13;  Length 128;
  Best Local Similarity   66.3%;  Pred. No. 1.6e-36;
  Matches   69;  Conservative   11;  Mismatches   24;  Indels    0;  Gaps    0;

Qy           2 QDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 61
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:10 ; Search time 29.8597 Seconds
(without alignments)
1109.503 Million cell updates/sec

Title: US-09-961-400-8
Perfect score: 584
Sequence: 1 MQDWLTFQKKHLTNTRDVDC.....TFCVTCENQAPVHFVGVGHC 105

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	565	96.7	127	13	Q9I8V8	Q9i8v8 rana pipien
2	543	93.0	127	13	Q8UVX5	Q8uvx5 rana pipien
3	391.5	67.0	129	13	Q9DFY6	Q9dfy6 rana catesb
4	382	65.4	128	13	Q9DFY8	Q9dfy8 rana catesb
5	307	52.6	128	13	Q9DFY7	Q9dfy7 rana catesb
6	305	52.2	128	13	Q9DFY5	Q9dfy5 rana catesb
7	292	50.0	133	13	Q98SM0	Q98sm0 rana catesb
8	279	47.8	132	13	Q98SM2	Q98sm2 rana catesb
9	276	47.3	133	13	Q98SL9	Q98sl9 rana catesb
10	272	46.6	133	13	Q98SL8	Q98sl8 rana catesb
11	270	46.2	132	13	Q98SM1	Q98sm1 rana catesb
12	265.5	45.5	132	13	Q9DF78	Q9df78 rana catesb
13	154.5	26.5	169	13	Q9W738	Q9w738 xenopus lae
14	120	20.5	157	11	Q9JKJ3	Q9jkj3 meriones un
15	120	20.5	157	11	Q9JKI9	Q9jki9 meriones un
16	119.5	20.5	146	6	Q861Y3	Q861y3 pygathrix r
17	119.5	20.5	146	6	Q861Y2	Q861y2 pygathrix b
18	119.5	20.5	146	6	Q861Y1	Q861y1 pygathrix a
19	118	20.2	157	11	Q9JKJ4	Q9jkj4 meriones un
20	117	20.0	157	11	Q9JKJ2	Q9jkj2 meriones un
21	116	19.9	152	11	Q9JKI5	Q9jki5 mus saxicol
22	115.5	19.8	153	11	Q9JKI7	Q9jki7 mus saxicol
23	115	19.7	147	6	Q7YRJ5	Q7yrj5 tursiops tr
24	115	19.7	157	11	Q9JKJ1	Q9jkj1 meriones un
25	114.5	19.6	146	6	Q861Y4	Q861y4 trachypithe
26	113.5	19.4	132	6	Q9TV24	Q9tv24 galago moho
27	113	19.3	147	6	Q7YRJ6	Q7yrj6 balaena mys
28	111.5	19.1	119	6	Q9TSQ6	Q9tsq6 cercopithec
29	111.5	19.1	119	6	Q9TV32	Q9tv32 gorilla gor
30	111.5	19.1	147	6	Q8HZQ0	Q8hzq0 pan troglod
31	110.5	18.9	119	6	Q9TV30	Q9tv30 saguinus oe
32	110	18.8	154	11	Q9JKI8	Q9jki8 mus saxicol
33	109.5	18.8	155	11	Q9JKH9	Q9jkh9 mus pahari
34	108.5	18.6	132	6	Q9TV25	Q9tv25 eulemur ful
35	108.5	18.6	155	11	Q9JKI3	Q9jki3 mus saxicol
36	108	18.5	124	6	Q95NE6	Q95ne6 bubalus bub
37	108	18.5	146	6	Q861Y5	Q861y5 colobus gue
38	106.5	18.2	155	11	Q9JKH8	Q9jkh8 mus pahari
39	106.5	18.2	170	6	Q9BEC1	Q9bec1 tragulus ja
40	106	18.2	144	6	Q9BH14	Q9bh14 antilocapra
41	105.5	18.1	144	11	Q80Z85	Q80z85 mus musculu
42	105.5	18.1	153	11	Q80XS4	Q80xs4 mus musculu
43	105.5	18.1	155	11	Q9JKI6	Q9jki6 mus saxicol
44	104.5	17.9	119	6	Q9TV31	Q9tv31 saimiri sci
45	104.5	17.9	155	11	Q9JKI2	Q9jki2 mus saxicol

ALIGNMENTS

RESULT 1
Q9I8V8
ID Q9I8V8 PRELIMINARY; PRT; 127 AA.
AC Q9I8V8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Onconase variant rapLR1 precursor.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20330357; PubMed=10871370;
RA Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;
RT "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a
RT 3' UTR of unusual length and structure.";
RL Nucleic Acids Res. 28:2375-2382(2000).
DR EMBL; AF165133; AAF76935.1; -.
DR PIR; A39035; A39035.
DR HSSP; P22069; 1ONC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNAse_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
SQ SEQUENCE 127 AA; 14491 MW; B8511DC5407AB69B CRC64;

Query Match 96.7%; Score 565; DB 13; Length 127;
Best Local Similarity 97.1%; Pred. No. 8.7e-58;
Matches 101; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 61

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Q861Y3
ID   Q861Y3      PRELIMINARY;      PRT;   146 AA.
AC   Q861Y3;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Angiogenin.
OS   Pygathrix roxellana (golden snub-nosed monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC   Pygathrix.
OX   NCBI_TaxID=61622;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22597544; PubMed=12711394;
RA   Zhang J., Zhang Y.-P.;
RT   "Pseudogenization of the tumor-growth promoter angiogenin in a leaf-
RT   eating monkey.";
RL   Gene 308:95-101(2003).
DR   EMBL; AY221130; AAO41337.1; -.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
SQ   SEQUENCE   146 AA;  16438 MW;  8CF170A4BD12BA67 CRC64;

  Query Match             22.2%;  Score 129.5;  DB 6;  Length 146;
  Best Local Similarity   34.2%;  Pred. No. 4.2e-07;
  Matches   38;  Conservative   16;  Mismatches   40;  Indels   17;  Gaps    7;

Qy          2 QDWLTFQKKHLTNT----RDVDCNNIMSTN--LFHCKDKNTFIYSRPEPVKAIC---KGI 52
              :|:||   ||   |     |  | ::|        ||| ||||:     :||||    |
Db         31 RDFLT---KHYDATPQGRNDRYCESMMRRRGLTSPCKDINTFIHGNSRHIKAICGDENGN 87

Qy         53 IASKNV-LTTSEFYLSDCNV---TSR-PCKYKLKKSTNTFCVTCENQAPVH 98
                :|: :: | | :: ||:   :|| ||:|:         | |||  |||
Db         88 PYGENLRISKSPFQVTTCNLRGGSSRPPCRYRATAGFRNIVVACENDLPVH 138


RESULT 15
Q861Y2
ID   Q861Y2      PRELIMINARY;      PRT;   146 AA.
AC   Q861Y2;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Angiogenin.
OS   Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC   Pygathrix.
OX   NCBI_TaxID=61621;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22597544; PubMed=12711394;
RA   Zhang J., Zhang Y.-P.;
RT   "Pseudogenization of the tumor-growth promoter angiogenin in a leaf-
RT   eating monkey.";
RL   Gene 308:95-101(2003).
DR   EMBL; AY221131; AAO41338.1; -.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
SQ   SEQUENCE   146 AA;  16438 MW;  8CF170A4BD12BA67 CRC64;

  Query Match             22.2%;  Score 129.5;  DB 6;  Length 146;
  Best Local Similarity   34.2%;  Pred. No. 4.2e-07;
  Matches   38;  Conservative   16;  Mismatches   40;  Indels   17;  Gaps    7;

Qy          2 QDWLTFQKKHLTNT----RDVDCNNIMSTN--LFHCKDKNTFIYSRPEPVKAIC---KGI 52
              :|:||   ||   |     |  | ::|        ||| ||||:     :||||    |
Db         31 RDFLT---KHYDATPQGRNDRYCESMMRRRGLTSPCKDINTFIHGNSRHIKAICGDENGN 87

Qy         53 IASKNV-LTTSEFYLSDCNV---TSR-PCKYKLKKSTNTFCVTCENQAPVH 98
                :|: :: | | :: ||:   :|| ||:|:         | |||  |||
Db         88 PYGENLRISKSPFQVTTCNLRGGSSRPPCRYRATAGFRNIVVACENDLPVH 138


Search completed: May  7, 2004, 21:46:01
Job time : 29.8597 secs
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RESULT 11
Q98SM1
ID   Q98SM1      PRELIMINARY;      PRT;   132 AA.
AC   Q98SM1;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RNase A-type ribonuclease rc204 precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21539506; PubMed=11683320;
RA   Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT   "Rapid diversification of RNase A superfamily ribonuclease from the
RT   bullfrog, Rana catesbeiana.";
RL   J. Mol. Evol. 53:31-38(2001).
DR   EMBL; AF351208; AAK30254.1; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     22       POTENTIAL.
SQ   SEQUENCE   132 AA;  14704 MW;  95D61760F729868E CRC64;

  Query Match             48.0%;  Score 280;  DB 13;  Length 132;
  Best Local Similarity   48.6%;  Pred. No. 1.4e-24;
  Matches   54;  Conservative   14;  Mismatches   35;  Indels    8;  Gaps    3;

Qy          2 QDWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 57
              ||| |||:||: :|  :||| ||  :::     ||  ||||      |||||  |:: | |
Db         23 QDWPTFQQKHIPSTSSIDCNTIMDKDIYIVRGQCKKVNTFIIYSATTVKAICTGVLNS-N 81

Qy         58 VLTTSEFYLSDCN---VTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
              ||:|: | |       :|||||  |   | ||  || |||: |||| |:| |
Db         82 VLSTTRFQLXXXTRTFITSRPCPYSSTKETNKICVKCENEYPVHFAGIGKC 132


RESULT 12
Q9DF78
ID   Q9DF78      PRELIMINARY;      PRT;   132 AA.
AC   Q9DF78;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RC-RNaseL1 ribonuclease precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20512555; PubMed=11058105;
RA   Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT   "Purification and cloning of cytotoxic ribonucleases from Rana
RT   catesbeiana (bullfrog).";
RL   Nucleic Acids Res. 28:4097-4104(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF288642; AAG30414.2; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    132       RC-RNASEL1 RIBONUCLEASE.
SQ   SEQUENCE   132 AA;  14625 MW;  D8D9A517452FBE53 CRC64;

  Query Match             47.3%;  Score 275.5;  DB 13;  Length 132;
  Best Local Similarity   44.1%;  Pred. No. 4.6e-24;
  Matches   49;  Conservative   19;  Mismatches   36;  Indels    7;  Gaps    2;

Qy          2 QDWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 57
              |:|  |::||:|:|  :||| ||   ::     ||::|||| |  : ||||| |:  :
Db         22 QNWAKFKEKHITSTSSIDCNTIMDKAIYIVGGKCKERNTFIISSEDNVKAICSGVSPDRK 81

Qy         58 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
              |:|: | |: |   ::| ||| |     |  || || | ||||||:| |
Db         82 ELSTTSFKLNTCIRDSITPRPCPYHPSPDNNKICVKCEKQLPVHFVGIGKC 132


RESULT 13
Q9W738
ID   Q9W738      PRELIMINARY;      PRT;   169 AA.
AC   Q9W738;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   FRL2 protein.
GN   FRL2.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96069863; PubMed=7585965;
RA   Kinoshita N., Minshull J., Kirschner M.W.;
RT   "The identification of two novel ligands of the FGF receptor by a
RT   yeast screening method and their activity in Xenopus development.";
RL   Cell 83:621-630(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Kinoshita N., Kirschner M.W.;
RL   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF159166; AAD41901.1; -.
DR   HSSP; P00656; 1LSQ.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
SQ   SEQUENCE   169 AA;  18891 MW;  D969F3E43B3CE1B8 CRC64;

  Query Match             27.0%;  Score 157.5;  DB 13;  Length 169;
  Best Local Similarity   36.1%;  Pred. No. 2.8e-10;
  Matches   39;  Conservative   19;  Mismatches   35;  Indels   15;  Gaps    6;

Qy          7 FQKKHLTNT-RDVDCN------NIMSTNLFHCKDKNTFIY-SRPEPVKAICKGIIASKNV 58
              | :||:     : :||       ||    |  :|| :|||: :  : || :| ||: |  |
Db         33 FMEKHIVKEGAETNCNQTIKDRNIRFKN--NCKFRNTFIHDTNGKKVKEMCAGIVKSTFV 90

Qy         59 LTTSEFYLSDCNV---TSRP--CKYKLKKSTNTFCVTCENQAPVHFVG 101
              ::      |:|| :   |:||  | |   ::|    :|||| |||| |
Db         91 ISKELLPLTDCLLMGRTARPPNCAYNQTRTTGVINITCENNYPVHFAG 138


RESULT 14
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                ||:|: | |: |   ::| ||| |  :   |  || |||| |||| |:| |
Db         82 VLSTTRFQLNTCTRTSITPRPCPYSSRTENNYICVKCENQYPVHFAGIGRC 132


RESULT 8
Q98SL9
ID   Q98SL9      PRELIMINARY;      PRT;   133 AA.
AC   Q98SL9;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RNase A-type ribonuclease rc212 precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21539506; PubMed=11683320;
RA   Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT   "Rapid diversification of RNase A superfamily ribonuclease from the
RT   bullfrog, Rana catesbeiana.";
RL   J. Mol. Evol. 53:31-38(2001).
DR   EMBL; AF351210; AAK30256.1; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     22       POTENTIAL.
SQ   SEQUENCE   133 AA;  14615 MW;  C8785B236B26E54E CRC64;

  Query Match             49.1%;  Score 286;  DB 13;  Length 133;
  Best Local Similarity   47.7%;  Pred. No. 2.8e-25;
  Matches   53;  Conservative   17;  Mismatches   33;  Indels    8;  Gaps    3;

Qy          2 QDWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 57
              |:| |||:||:|||  ::|:|||: :|:     ||  |||| |    || || | :  |
Db         23 QNWATFQQKHITNTSSINCSNIMNNSLYIVGGQCKKVNTFIASSATTVKGICSG-VTDKK 81

Qy         58 VLTTSEFYLSDCN---VTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
              ||::::| |  |    :| ||| |  :  ||  || |||| |||| |:| |
Db         82 VLSSTKFQLDICTRIFITPRPCPYSSRTETNYICVKCENQYPVHFAGIGQC 132


RESULT 9
Q98SM2
ID   Q98SM2      PRELIMINARY;      PRT;   132 AA.
AC   Q98SM2;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21539506; PubMed=11683320;
RA   Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT   "Rapid diversification of RNase A superfamily ribonuclease from the
RT   bullfrog, Rana catesbeiana.";
RL   J. Mol. Evol. 53:31-38(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Tang P.-C., Jeng J.-T.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF351207; AAK30253.1; -.
DR   EMBL; AF359578; AAL87036.1; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     22       POTENTIAL.
FT   CHAIN        23    132       RC-RNASE7.
SQ   SEQUENCE   132 AA;  14412 MW;  131A745187978687 CRC64;

  Query Match             48.9%;  Score 285;  DB 13;  Length 132;
  Best Local Similarity   47.7%;  Pred. No. 3.7e-25;
  Matches   53;  Conservative   14;  Mismatches   36;  Indels    8;  Gaps    3;

Qy          2 QDWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 57
              | |  ||:||: :|  ::|| ||  |::     ||  |||| |    ||||| | : : |
Db         23 QTWAKFQQKHIPSTSSINCNTIMDNNIYIVGGQCKKVNTFIISSATTVKAICNG-VTNSN 81

Qy         58 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
              ||: : | |  |   ::| ||| |  || ||  || |||| |||| |:| |
Db         82 VLSPTRFQLDTCTRTSITPRPCPYSSKKETNKICVKCENQLPVHFAGIGKC 132


RESULT 10
Q98SL8
ID   Q98SL8      PRELIMINARY;      PRT;   133 AA.
AC   Q98SL8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RNase A-type ribonuclease rc218 precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21539506; PubMed=11683320;
RA   Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT   "Rapid diversification of RNase A superfamily ribonuclease from the
RT   bullfrog, Rana catesbeiana.";
RL   J. Mol. Evol. 53:31-38(2001).
DR   EMBL; AF351211; AAK30257.1; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     22       POTENTIAL.
SQ   SEQUENCE   133 AA;  14590 MW;  8B40B9A94FA5B943 CRC64;

  Query Match             48.4%;  Score 282;  DB 13;  Length 133;
  Best Local Similarity   46.8%;  Pred. No. 8.2e-25;
  Matches   52;  Conservative   18;  Mismatches   33;  Indels    8;  Gaps    3;

Qy          2 QDWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 57
              |:| |||::|:|||  ::|:|||: :|:     ||  |||| |    || || | :  |
Db         23 QNWATFQEQHITNTSSINCSNIMNNSLYIVGGQCKKVNTFIASSATTVKGICSG-VTDKK 81

Qy         58 VLTTSEFYLSDCN---VTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
              ||::::| |  |    :| ||| |  :  ||  || |||| |||| |:| |
Db         82 VLSSTKFQLDICTRIFITPRPCPYSSRTETNYICVKCENQYPVHFAGIGQC 132
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Db         24 QNWETFQKKHLTDTRDVKCDAEMKKALFDCKQKNTFIYARPGRVQALCKNIIVSKNVLST 83

Qy         62 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
Db         84 DEFYLSDCNRIKLPCHYKLKKSSNTICITCENKLPVHFVAVEEC 127


RESULT 5
Q9DFY7
ID   Q9DFY7      PRELIMINARY;      PRT;   128 AA.
AC   Q9DFY7;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RC-RNase3 ribonuclease precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20512555; PubMed=11058105;
RA   Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT   "Purification and cloning of cytotoxic ribonucleases from Rana
RT   catesbeiana (bullfrog).";
RL   Nucleic Acids Res. 28:4097-4104(2000).
DR   EMBL; AF242554; AAG31440.2; -.
DR   HSSP; P22069; 1ONC.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24    128       RC-RNASE3 RIBONUCLEASE.
SQ   SEQUENCE   128 AA;  14517 MW;  2B14986082E0587D CRC64;

  Query Match             53.3%;  Score 311;  DB 13;  Length 128;
  Best Local Similarity   54.8%;  Pred. No. 3.5e-28;
  Matches   57;  Conservative   12;  Mismatches   35;  Indels    0;  Gaps    0;

Qy          2 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 61
Db         24 QDWETFQKKHLTDTKKVKCDVEMAKALFDCKKTNTFIYALPGRVKALCKNIRDNTDVLSR 83

Qy         62 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
Db         84 DAFLLPQCDRIKLPCHYKLSSSTNTICITCVNQLPIHFAGVGSC 127


RESULT 6
Q9DFY5
ID   Q9DFY5      PRELIMINARY;      PRT;   128 AA.
AC   Q9DFY5;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RC-RNase6 ribonuclease precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20512555; PubMed=11058105;
RA   Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT   "Purification and cloning of cytotoxic ribonucleases from Rana
RT   catesbeiana (bullfrog).";
RL   Nucleic Acids Res. 28:4097-4104(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF242556; AAG31442.2; -.
DR   HSSP; P22069; 1ONC.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24    128       RC-RNASE6 RIBONUCLEASE.
SQ   SEQUENCE   128 AA;  14804 MW;  AFEBFD67D266C7C2 CRC64;

  Query Match             53.0%;  Score 309;  DB 13;  Length 128;
  Best Local Similarity   53.8%;  Pred. No. 5.9e-28;
  Matches   56;  Conservative   13;  Mismatches   35;  Indels    0;  Gaps    0;

Qy          2 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 61
Db         24 QDWDTFQKKHLTDTKKVKCDVEMKKALFDCKKTNTFIFARPPRVQALCKNIKDNTNVLSR 83

Qy         62 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
Db         84 DVFYLPQCNRKKLPCHYRLDGSTNTICLTCMKELPIHFAGVGKC 127


RESULT 7
Q98SM0
ID   Q98SM0      PRELIMINARY;      PRT;   133 AA.
AC   Q98SM0;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RNase A-type ribonuclease rc208 precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21539506; PubMed=11683320;
RA   Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT   "Rapid diversification of RNase A superfamily ribonuclease from the
RT   bullfrog, Rana catesbeiana.";
RL   J. Mol. Evol. 53:31-38(2001).
DR   EMBL; AF351209; AAK30255.1; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     22       POTENTIAL.
SQ   SEQUENCE   133 AA;  14628 MW;  87FCF122C3499E02 CRC64;

  Query Match             51.1%;  Score 298;  DB 13;  Length 133;
  Best Local Similarity   49.5%;  Pred. No. 1.2e-26;
  Matches   55;  Conservative   16;  Mismatches   32;  Indels    8;  Gaps    3;

Qy          2 QDWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 57
Db         23 QNWATFQQKHITNTSSINCNTIMDNNIYIVGGQCKGVNTFIISSATTVKAICTGVI-NMN 81

Qy         58 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          24 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 83

Qy          62 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                    |||||||||||||||||||||||||||||||||||||||||
Db          84 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 127


RESULT 2
Q8UVX5
ID   Q8UVX5      PRELIMINARY;      PRT;   127 AA.
AC   Q8UVX5;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Onconase precursor.
GN   RPR.
OS   Rana pipiens (Northern leopard frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8404;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Liao Y.-D., Wang S.-C.;
RT   "Rana pipiens onconase genomic DNA.";
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF332139; AAL54383.1; -.
DR   PIR; A39035; A39035.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     23       POTENTIAL.
SQ   SEQUENCE   127 AA;  14469 MW;  953F90D351CFEEF3 CRC64;

  Query Match             95.4%;  Score 556;  DB 13;  Length 127;
  Best Local Similarity   96.2%;  Pred. No. 1.4e-56;
  Matches  100;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy           2 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 61
                 ||||||||||:||||||||:||||||||||||||||||||||||||||||||||||||||
Db          24 QDWLTFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 83

Qy          62 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                 |||||||||||||||||||||| |||||||||||||||| |
Db          84 SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 127


RESULT 3
Q9DFY6
ID   Q9DFY6      PRELIMINARY;      PRT;   129 AA.
AC   Q9DFY6;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RC-RNase4 ribonuclease precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20512555; PubMed=11058105;
RA   Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT   "Purification and cloning of cytotoxic ribonucleases from Rana
RT   catesbeiana (bullfrog).";
RL   Nucleic Acids Res. 28:4097-4104(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF242555; AAG31441.2; -.
DR   PDB; 1KVZ; 28-JUL-02.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24    129       RC-RNASE4 RIBONUCLEASE.
SQ   SEQUENCE   129 AA;  14724 MW;  826A62882B10ABDA CRC64;

  Query Match             69.4%;  Score 404.5;  DB 13;  Length 129;
  Best Local Similarity   67.6%;  Pred. No. 5.1e-39;
  Matches   71;  Conservative   16;  Mismatches   17;  Indels    1;  Gaps    1;

Qy           2 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 61
                 ||| ||:|||||:| ||||:|:| |:|| ||||||||||| | ||||:|:|:| | :||:
Db          24 QDWATFKKKHLTDTWDVDCDNLMPTSLFDCKDKNTFIYSLPGPVKALCRGVIFSADVLSN 83

Qy          62 SEFYLSDCNVTSR-PCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                 |||||::|||  | ||||||||||:|  |: ||:: |||| ||| |
Db          84 SEFYLAECNVKPRKPCKYKLKKSSNRICIRCEHELPVHFAGVGIC 128


RESULT 4
Q9DFY8
ID   Q9DFY8      PRELIMINARY;      PRT;   128 AA.
AC   Q9DFY8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RC-RNase2 ribonuclease precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20512555; PubMed=11058105;
RA   Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT   "Purification and cloning of cytotoxic ribonucleases from Rana
RT   catesbeiana (bullfrog).";
RL   Nucleic Acids Res. 28:4097-4104(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF242553; AAG31439.1; -.
DR   PDB; 1M58; 09-JAN-03.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24    128       RC-RNASE2 RIBONUCLEASE.
SQ   SEQUENCE   128 AA;  14839 MW;  989719CF52053ECC CRC64;

  Query Match             66.2%;  Score 386;  DB 13;  Length 128;
  Best Local Similarity   67.3%;  Pred. No. 7.1e-37;
  Matches   70;  Conservative   10;  Mismatches   24;  Indels    0;  Gaps    0;

Qy           2 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 61
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:10 ; Search time 29.8597 Seconds
(without alignments)
1109.503 Million cell updates/sec

Title: US-09-961-400-6
Perfect score: 583
Sequence: 1 MQDWLTFQKKHLTNTRDVDC.....TFCVTCENQAPVHFVGVGHC 105

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	578	99.1	127	13	Q9I8V8	Q9i8v8 rana pipien
2	556	95.4	127	13	Q8UVX5	Q8uvx5 rana pipien
3	404.5	69.4	129	13	Q9DFY6	Q9dfy6 rana catesb
4	386	66.2	128	13	Q9DFY8	Q9dfy8 rana catesb
5	311	53.3	128	13	Q9DFY7	Q9dfy7 rana catesb
6	309	53.0	128	13	Q9DFY5	Q9dfy5 rana catesb
7	298	51.1	133	13	Q98SM0	Q98sm0 rana catesb
8	286	49.1	133	13	Q98SL9	Q98sl9 rana catesb
9	285	48.9	132	13	Q98SM2	Q98sm2 rana catesb
10	282	48.4	133	13	Q98SL8	Q98sl8 rana catesb
11	280	48.0	132	13	Q98SM1	Q98sm1 rana catesb
12	275.5	47.3	132	13	Q9DF78	Q9df78 rana catesb
13	157.5	27.0	169	13	Q9W738	Q9w738 xenopus lae
14	129.5	22.2	146	6	Q861Y3	Q861y3 pygathrix r
15	129.5	22.2	146	6	Q861Y2	Q861y2 pygathrix b
16	129.5	22.2	146	6	Q861Y1	Q861y1 pygathrix a
17	129	22.1	152	11	Q9JKI5	Q9jki5 mus saxicol
18	127	21.8	157	11	Q9JKI9	Q9jki9 meriones un
19	126.5	21.7	153	11	Q9JKI7	Q9jki7 mus saxicol
20	126	21.6	157	11	Q9JKJ3	Q9jkj3 meriones un
21	125.5	21.5	146	6	Q861Y4	Q861y4 trachypithe
22	125	21.4	157	11	Q9JKJ4	Q9jkj4 meriones un
23	123	21.1	154	11	Q9JKI8	Q9jki8 mus saxicol
24	122	20.9	157	11	Q9JKJ1	Q9jkj1 meriones un
25	121	20.8	147	6	Q7YRJ6	Q7yrj6 balaena mys
26	121	20.8	157	11	Q9JKJ2	Q9jkj2 meriones un
27	120.5	20.7	155	11	Q9JKH9	Q9jkh9 mus pahari
28	119.5	20.5	155	11	Q9JKI3	Q9jki3 mus saxicol
29	118	20.2	147	6	Q7YRJ5	Q7yrj5 tursiops tr
30	116.5	20.0	155	11	Q9JKI6	Q9jki6 mus saxicol
31	115.5	19.8	132	6	Q9TV25	Q9tv25 eulemur ful
32	115.5	19.8	155	11	Q9JKI2	Q9jki2 mus saxicol
33	115.5	19.8	155	11	Q9JKI4	Q9jki4 mus saxicol
34	115	19.7	146	6	Q861Y5	Q861y5 colobus gue
35	114.5	19.6	132	6	Q9TV24	Q9tv24 galago moho
36	114.5	19.6	170	6	Q9BEC1	Q9bec1 tragulus ja
37	113.5	19.5	119	6	Q9TSQ6	Q9tsq6 cercopithec
38	113.5	19.5	119	6	Q9TV32	Q9tv32 gorilla gor
39	113.5	19.5	147	6	Q8HZQ0	Q8hzq0 pan troglod
40	113.5	19.5	155	11	Q9R134	Q9r134 rattus norv
41	113	19.4	156	11	Q9JKG6	Q9jkg6 mus caroli
42	113	19.4	156	11	Q9JKH7	Q9jkh7 mus caroli
43	112.5	19.3	119	6	Q9TV30	Q9tv30 saguinus oe
44	112.5	19.3	155	11	Q9R125	Q9r125 mus musculu
45	112.5	19.3	155	11	Q9JKH8	Q9jkh8 mus pahari

ALIGNMENTS

RESULT 1
Q9I8V8
ID Q9I8V8 PRELIMINARY; PRT; 127 AA.
AC Q9I8V8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Onconase variant rapLR1 precursor.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20330357; PubMed=10871370;
RA Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;
RT "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a
RT 3' UTR of unusual length and structure.";
RL Nucleic Acids Res. 28:2375-2382(2000).
DR EMBL; AF165133; AAF76935.1; -.
DR PIR; A39035; A39035.
DR HSSP; P22069; 1ONC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNAse_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
SQ SEQUENCE 127 AA; 14491 MW; B8511DC5407AB69B CRC64;

Query Match 99.1%; Score 578; DB 13; Length 127;
Best Local Similarity 100.0%; Pred. No. 4e-59;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 61

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Q9JKJ3
ID   Q9JKJ3      PRELIMINARY;      PRT;   157 AA.
AC   Q9JKJ3;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Eosinophil-associated ribonuclease 25.
GN   EAR25.
OS   Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC   Meriones.
OX   NCBI_TaxID=10047;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20243759; PubMed=10758160;
RA   Zhang J., Dyer K.D., Rosenberg H.F.;
RT   "Evolution of the rodent eosinophil-associated ribonuclease gene
RT   family by rapid gene sorting and positive selection.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:4701-4706(2000).
DR   EMBL; AF238390; AAF67690.1; -.
DR   HSSP; P10153; 1HI2.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
SQ   SEQUENCE   157 AA;  17945 MW;  FDFE22FE77FE371A CRC64;

  Query Match          21.1%;  Score 122;  DB 11;  Length 157;
  Best Local Similarity   29.2%;  Pred. No. 3.4e-06;
  Matches   33;  Conservative   19;  Mismatches   33;  Indels   28;  Gaps    6;

Qy          3 WLTFQKKHLTNTRDVDCN-NILSTNLF--HCKDKNTFIYSRPEPVKAICKGIIASKNVLT 59
              | | |  |::||  : ||  :|  | :   ||| |||:::|   |   |       | |
Db         36 WFTIQ--HISNTTTIQCNAAMLGVNNYTGRCKDLNTFLHTRFANVVNEC------YNRNT 87

Qy         60 TFE----------FYLSDCNVTS-----RPCKYKLKKSTNTFCVTCENQAP 95
              | :             ::|||:||     | |:|:  ::   : : | |: |
Db         88 TCKNGRRNCHDSRSRVSITDCNLTSPSTNYRQCRYQRTRARKFYRIACNNKTP 140


RESULT 15
Q9JKI9
ID   Q9JKI9      PRELIMINARY;      PRT;   157 AA.
AC   Q9JKI9;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Eosinophil-associated ribonuclease 44.
GN   EAR44.
OS   Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC   Meriones.
OX   NCBI_TaxID=10047;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20243759; PubMed=10758160;
RA   Zhang J., Dyer K.D., Rosenberg H.F.;
RT   "Evolution of the rodent eosinophil-associated ribonuclease gene
RT   family by rapid gene sorting and positive selection.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:4701-4706(2000).
DR   EMBL; AF238394; AAF67694.1; -.
DR   HSSP; P10153; 1HI2.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
SQ   SEQUENCE   157 AA;  17887 MW;  34FE2AE777EF3709 CRC64;

  Query Match          21.1%;  Score 122;  DB 11;  Length 157;
  Best Local Similarity   29.4%;  Pred. No. 3.4e-06;
  Matches   32;  Conservative   21;  Mismatches   36;  Indels   20;  Gaps    7;

Qy          3 WLTFQKKHLTNTRDVDCN-NILSTNLF--HCKDKNTFIYSRPEPV-------KAICKGII 52
              | | |  |::||  : ||  :|  | :   ||| |||:::|   |           ||
Db         36 WFTIQ--HISNTTTIQCNAAMLGVNNYTGRCKDLNTFLHTRFANVVNECYNRNTTCKN-- 91

Qy         53 ASKNVL-TTFEFYLSDCNVTS-----RPCKYKLKKSTNTFCVTCENQAP 95
                :|   :  :  ::|||:||     | |:|:  ::   : : | |: |
Db         92 GRRNCHDSRSKVSITDCNLTSPSANYRQCRYQRTRARKFYRIACNNKTP 140


Search completed: May  7, 2004, 21:46:01
Job time : 29.5753 secs
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RESULT 11
Q98SM1
ID   Q98SM1      PRELIMINARY;      PRT;   132 AA.
AC   Q98SM1;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RNase A-type ribonuclease rc204 precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21539506; PubMed=11683320;
RA   Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT   "Rapid diversification of RNase A superfamily ribonuclease from the
RT   bullfrog, Rana catesbeiana.";
RL   J. Mol. Evol. 53:31-38(2001).
DR   EMBL; AF351208; AAK30254.1; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     22       POTENTIAL.
SQ   SEQUENCE   132 AA;  14704 MW;  95D61760F729868E CRC64;

  Query Match             47.3%;  Score 274;  DB 13;  Length 132;
  Best Local Similarity   47.7%;  Pred. No. 7.1e-24;
  Matches   53;  Conservative   14;  Mismatches   36;  Indels    8;  Gaps    3;

Qy          1 QDWLTFQKKHLTNTRDVDCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56
              ||| |||:||: :|  :||| |:  :::     ||  ||||      |||||  |:: | |
Db         23 QDWPTFQQKHIPSTSSIDCNTIMDKDIYIVRGQCKKVNTFIIYSATTVKAICTGVLNS-N 81

Qy         57 VLTTFEFYLSDCN---VTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
              ||:|  | |       :||||| |   | ||  || |||: |||| |:| |
Db         82 VLSTTRFQLXXXTRTFITSRPCPYSSTKETNKICVKCENEYPVHFAGIGKC 132


RESULT 12
Q9DF78
ID   Q9DF78      PRELIMINARY;      PRT;   132 AA.
AC   Q9DF78;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RC-RNaseL1 ribonuclease precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20512555; PubMed=11058105;
RA   Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT   "Purification and cloning of cytotoxic ribonucleases from Rana
RT   catesbeiana (bullfrog).";
RL   Nucleic Acids Res. 28:4097-4104(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF288642; AAG30414.2; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    132       RC-RNASEL1 RIBONUCLEASE.
SQ   SEQUENCE   132 AA;  14625 MW;  D8D9A517452FBE53 CRC64;

  Query Match             46.5%;  Score 269.5;  DB 13;  Length 132;
  Best Local Similarity   43.2%;  Pred. No. 2.4e-23;
  Matches   48;  Conservative   19;  Mismatches   37;  Indels    7;  Gaps    2;

Qy          1 QDWLTFQKKHLTNTRDVDCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56
              |:|  |::||:|:|  :||| |:   ::      ||::|||| |  : |||||  |:   :
Db         22 QNWAKFKEKHITSTSSIDCNTIMDKAIYIVGGKCKERNTFIISSEDNVKAICSGVSPDRK 81

Qy         57 VLTTFEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
              |:|  | |: |   ::| ||| |       |  || || | |||||:| |
Db         82 ELSTTSFKLNTCIRDSITPRPCPYHPSPDNNKICVKCEKQLPVHFVGIGKC 132


RESULT 13
Q9W738
ID   Q9W738      PRELIMINARY;      PRT;   169 AA.
AC   Q9W738;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   FRL2 protein.
GN   FRL2.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96069863; PubMed=7585965;
RA   Kinoshita N., Minshull J., Kirschner M.W.;
RT   "The identification of two novel ligands of the FGF receptor by a
RT   yeast screening method and their activity in Xenopus development.";
RL   Cell 83:621-630(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Kinoshita N., Kirschner M.W.;
RL   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF159166; AAD41901.1; -.
DR   HSSP; P00656; 1LSQ.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
SQ   SEQUENCE   169 AA;  18891 MW;  D969F3E43B3CE1B8 CRC64;

  Query Match             26.5%;  Score 153.5;  DB 13;  Length 169;
  Best Local Similarity   36.1%;  Pred. No. 8.3e-10;
  Matches   39;  Conservative   19;  Mismatches   35;  Indels   15;  Gaps    6;

Qy          6 FQKKHLTNT-RDVDCN------NILSTNLFHCKDKNTFIY-SRPEPVKAICKGIIASKNV 57
              | :||:     : :||      ||   |  :|| :||||: :  : || :| ||: |  |
Db         33 FMEKHIVKEGAETNCNQTIKDRNIRFKN--NCKFRNTFIHDTNGKKVKEMCAGIVKSTFV 90

Qy         58 LTTFEFYLSDCNV---TSRP--CKYKLKKSTNTFCVTCENQAPVHFVG 100
              ::     |:|| :   |:||  | |   ::|   :|||| |||| |
Db         91 ISKELLPLTDCLLMGRTARPPNCAYNQTRTTGVINITCENNYPVHFAG 138


RESULT 14
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                ||:|  | |: |   ::| ||| |  :   |  || |||| |||| |:| |
Db         82 VLSTTRFQLNTCTRTSITPRPCPYSSRTENNYICVKCENQYPVHFAGIGRC 132


RESULT 8
Q98SL9
ID   Q98SL9      PRELIMINARY;      PRT;   133 AA.
AC   Q98SL9;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RNase A-type ribonuclease rc212 precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21539506; PubMed=11683320;
RA   Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT   "Rapid diversification of RNase A superfamily ribonuclease from the
RT   bullfrog, Rana catesbeiana.";
RL   J. Mol. Evol. 53:31-38(2001).
DR   EMBL; AF351210; AAK30256.1; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     22       POTENTIAL.
SQ   SEQUENCE   133 AA;  14615 MW;  C8785B236B26E54E CRC64;

  Query Match             48.4%;  Score 280;  DB 13;  Length 133;
  Best Local Similarity   46.8%;  Pred. No. 1.4e-24;
  Matches   52;  Conservative   17;  Mismatches   34;  Indels    8;  Gaps    3;

Qy          1 QDWLTFQKKHLTNTRDVDCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56
              |:| |||:||:|||  ::|:||:: :|:     ||  |||| |    || || | :  |
Db         23 QNWATFQQKHITNTSSINCSNIMNNSLYIVGGQCKKVNTFIASSATTVKGICSG-VTDKK 81

Qy         57 VLTTFEFYLSDCN---VTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
              ||:: :| |  |    :| ||| |  :  ||  || |||| |||| |:| |
Db         82 VLSSTKFQLDICTRIFITPRPCPYSSRTETNYICVKCENQYPVHFAGIGQC 132


RESULT 9
Q98SM2
ID   Q98SM2      PRELIMINARY;      PRT;   132 AA.
AC   Q98SM2;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21539506; PubMed=11683320;
RA   Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT   "Rapid diversification of RNase A superfamily ribonuclease from the
RT   bullfrog, Rana catesbeiana.";
RL   J. Mol. Evol. 53:31-38(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Tang P.-C., Jeng J.-T.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF351207; AAK30253.1; -.
DR   EMBL; AF359578; AAL87036.1; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     22       POTENTIAL.
FT   CHAIN        23    132       RC-RNASE7.
SQ   SEQUENCE   132 AA;  14412 MW;  131A745187978687 CRC64;

  Query Match             48.2%;  Score 279;  DB 13;  Length 132;
  Best Local Similarity   46.8%;  Pred. No. 1.9e-24;
  Matches   52;  Conservative   14;  Mismatches   37;  Indels    8;  Gaps    3;

Qy          1 QDWLTFQKKHLTNTRDVDCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56
              | |  ||:||: :|  ::|| |:  |::     ||  |||| |    ||||| | : |
Db         23 QTWAKFQQKHIPSTSSINCNTIMDNNIYIVGGQCKKVNTFIISSATTVKAICNG-VTNSN 81

Qy         57 VLTTFEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
              ||:   | |  |    ::| ||| |  || ||  || |||| |||| |:| |
Db         82 VLSPTRFQLDTCTRTSITPRPCPYSSKKETNKICVKCENQLPVHFAGIGKC 132


RESULT 10
Q98SL8
ID   Q98SL8      PRELIMINARY;      PRT;   133 AA.
AC   Q98SL8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RNase A-type ribonuclease rc218 precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21539506; PubMed=11683320;
RA   Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT   "Rapid diversification of RNase A superfamily ribonuclease from the
RT   bullfrog, Rana catesbeiana.";
RL   J. Mol. Evol. 53:31-38(2001).
DR   EMBL; AF351211; AAK30257.1; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     22       POTENTIAL.
SQ   SEQUENCE   133 AA;  14590 MW;  8B40B9A94FA5B943 CRC64;

  Query Match             47.7%;  Score 276;  DB 13;  Length 133;
  Best Local Similarity   45.9%;  Pred. No. 4.2e-24;
  Matches   51;  Conservative   18;  Mismatches   34;  Indels    8;  Gaps    3;

Qy          1 QDWLTFQKKHLTNTRDVDCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56
              |:| |||::|:|||  ::|:||:: :|:     ||  |||| |    || || | :  |
Db         23 QNWATFQEQHITNTSSINCSNIMNNSLYIVGGQCKKVNTFIASSATTVKGICSG-VTDKK 81

Qy         57 VLTTFEFYLSDCN---VTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
              ||:: :| |  |    :| ||| |  :  ||  || |||| |||| |:| |
Db         82 VLSSTKFQLDICTRIFITPRPCPYSSRTETNYICVKCENQYPVHFAGIGQC 132
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                |:| |||||||:|||| |:  :   || || ||||||:||  |:|:|| || |||||:|
Db          24 QNWETFQKKHLTDTRDVKCDAEMKKALFDCKQKNTFIYARPGRVQALCKNIIVSKNVLST 83

Qy          61 FEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
               ||||||||    || ||||||:|| |:||||: ||||| |  |
Db          84 DEFYLSDCNRIKLPCHYKLKKSSNTICITCENKLPVHFVAVEEC 127


RESULT 5
Q9DFY7
ID   Q9DFY7      PRELIMINARY;      PRT;   128 AA.
AC   Q9DFY7;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RC-RNase3 ribonuclease precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20512555; PubMed=11058105;
RA   Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT   "Purification and cloning of cytotoxic ribonucleases from Rana
RT   catesbeiana (bullfrog).";
RL   Nucleic Acids Res. 28:4097-4104(2000).
DR   EMBL; AF242554; AAG31440.2; -.
DR   HSSP; P22069; 1ONC.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24    128       RC-RNASE3 RIBONUCLEASE.
SQ   SEQUENCE   128 AA;  14517 MW;  2B14986082E0587D CRC64;

  Query Match             52.7%;  Score 305;  DB 13;  Length 128;
  Best Local Similarity   53.8%;  Pred. No. 1.8e-27;
  Matches   56;  Conservative   13;  Mismatches   35;  Indels    0;  Gaps    0;

Qy           1 QDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 60
               ||| ||||||||:|: | |:  ::  || ||  |||||: |  |||:|| |  : :||:
Db          24 QDWETFQKKHLTDTKKVKCDVEMAKALFDCKKTNTFIYALPGRVKALCKNIRDNTDVLSR 83

Qy          61 FEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                 | |  |:    || |||  |||| |:|| || |:|| ||| |
Db          84 DAFLLPQCDRIKLPCHYKLSSSTNTICITCVNQLPIHFAGVGSC 127


RESULT 6
Q9DFY5
ID   Q9DFY5      PRELIMINARY;      PRT;   128 AA.
AC   Q9DFY5;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RC-RNase6 ribonuclease precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20512555; PubMed=11058105;
RA   Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT   "Purification and cloning of cytotoxic ribonucleases from Rana
RT   catesbeiana (bullfrog).";
RL   Nucleic Acids Res. 28:4097-4104(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF242556; AAG31442.2; -.
DR   HSSP; P22069; 1ONC.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24    128       RC-RNASE6 RIBONUCLEASE.
SQ   SEQUENCE   128 AA;  14804 MW;  AFEBFD67D266C7C2 CRC64;

  Query Match             52.3%;  Score 303;  DB 13;  Length 128;
  Best Local Similarity   52.9%;  Pred. No. 3e-27;
  Matches   55;  Conservative   14;  Mismatches   35;  Indels    0;  Gaps    0;

Qy           1 QDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 60
               ||| ||||||||:|: | |:  :   || ||  ||||::||  |:|:|| |  : |||:
Db          24 QDWDTFQKKHLTDTKKVKCDVEMKKALFDCKKTNTFIFARPPRVQALCKNIKDNTNVLSR 83

Qy          61 FEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                 |||  ||     || |:|  |||| |:||  : |:|| ||| |
Db          84 DVFYLPQCNRKKLPCHYRLDGSTNTICLTCMKELPIHFAGVGKC 127


RESULT 7
Q98SM0
ID   Q98SM0      PRELIMINARY;      PRT;   133 AA.
AC   Q98SM0;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RNase A-type ribonuclease rc208 precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21539506; PubMed=11683320;
RA   Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT   "Rapid diversification of RNase A superfamily ribonuclease from the
RT   bullfrog, Rana catesbeiana.";
RL   J. Mol. Evol. 53:31-38(2001).
DR   EMBL; AF351209; AAK30255.1; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     22       POTENTIAL.
SQ   SEQUENCE   133 AA;  14628 MW;  87FCF122C3499E02 CRC64;

  Query Match             50.4%;  Score 292;  DB 13;  Length 133;
  Best Local Similarity   48.6%;  Pred. No. 5.9e-26;
  Matches   54;  Conservative   16;  Mismatches   33;  Indels    8;  Gaps    3;

Qy           1 QDWLTFQKKHLTNTRDVDCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56
               |:| |||:||:|||  ::|| |:  |::     ||  |||| |    |||||:|:| : |
Db          23 QNWATFQQKHITNTSSINCNTIMDNNIYIVGGQCKGVNTFIISSATTVKAICTGVI-NMN 81

Qy          57 VLTTFEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
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                  ||||||||||||||||||||||:||||||||||||||||||||||||||||||||||||||
Db          24 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 83

Qy          61 FEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                  |||||||||||||||||||||||||||||||||||||||||||
Db          84 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 127


RESULT 2
Q8UVX5
ID   Q8UVX5      PRELIMINARY;      PRT;   127 AA.
AC   Q8UVX5;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Onconase precursor.
GN   RPR.
OS   Rana pipiens (Northern leopard frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8404;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Liao Y.-D., Wang S.-C.;
RT   "Rana pipiens onconase genomic DNA.";
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF332139; AAL54383.1; -.
DR   PIR; A39035; A39035.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     23       POTENTIAL.
SQ   SEQUENCE   127 AA;  14469 MW;  953F90D351CFEEF3 CRC64;

  Query Match             94.5%;  Score 547;  DB 13;  Length 127;
  Best Local Similarity   94.2%;  Pred. No. 1.7e-55;
  Matches   98;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 QDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 60
              ||||||||||:||||||||:||:||||||||||||||||||||||||||||||||||||||
Db          24 QDWLTFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 83

Qy          61 FEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                  |||||||||||||||||||| |||||||||||||||||| |
Db          84 SEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 127


RESULT 3
Q9DFY6
ID   Q9DFY6      PRELIMINARY;      PRT;   129 AA.
AC   Q9DFY6;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RC-RNase4 ribonuclease precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20512555; PubMed=11058105;
RA   Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT   "Purification and cloning of cytotoxic ribonucleases from Rana
RT   catesbeiana (bullfrog).";
RL   Nucleic Acids Res. 28:4097-4104(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF242555; AAG31441.2; -.
DR   PDB; 1KVZ; 28-JUL-02.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24    129       RC-RNASE4 RIBONUCLEASE.
SQ   SEQUENCE   129 AA;  14724 MW;  826A62882B10ABDA CRC64;

  Query Match             68.3%;  Score 395.5;  DB 13;  Length 129;
  Best Local Similarity   65.7%;  Pred. No. 5.9e-38;
  Matches   69;  Conservative   17;  Mismatches   18;  Indels    1;  Gaps    1;

Qy          1 QDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 60
              ||| ||:||||:| ||||:|:: |:|| ||||||||| | ||||:|:|:| | :||:
Db          24 QDWATFKKKHLTDTWDVDCDNLMPTSLFDCKDKNTFIYSLPGPVKALCRGVIFSADVLSN 83

Qy          61 FEFYLSDCNVTSR-PCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                 ||||::|||  | |||||||||:|  |: ||:: |||| ||| |
Db          84 SEFYLAECNVKPRKPCKYKLKKSSNRICIRCEHELPVHFAGVGIC 128


RESULT 4
Q9DFY8
ID   Q9DFY8      PRELIMINARY;      PRT;   128 AA.
AC   Q9DFY8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RC-RNase2 ribonuclease precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20512555; PubMed=11058105;
RA   Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT   "Purification and cloning of cytotoxic ribonucleases from Rana
RT   catesbeiana (bullfrog).";
RL   Nucleic Acids Res. 28:4097-4104(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF242553; AAG31439.1; -.
DR   PDB; 1M58; 09-JAN-03.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24    128       RC-RNASE2 RIBONUCLEASE.
SQ   SEQUENCE   128 AA;  14839 MW;  989719CF52053ECC CRC64;

  Query Match             65.6%;  Score 380;  DB 13;  Length 128;
  Best Local Similarity   66.3%;  Pred. No. 3.7e-36;
  Matches   69;  Conservative   11;  Mismatches   24;  Indels    0;  Gaps    0;

Qy          1 QDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 60
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:10 ; Search time 29.5753 Seconds
(without alignments)
1109.503 Million cell updates/sec

Title: US-09-961-400-4
Perfect score: 579
Sequence: 1 QDWLTFQKKHLTNTRDVDCN.....TFCVTCENQAPVHFVGVGHC 104

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	569	98.3	127	13	Q9I8V8	Q9i8v8 rana pipien
2	547	94.5	127	13	Q8UVX5	Q8uvx5 rana pipien
3	395.5	68.3	129	13	Q9DFY6	Q9dfy6 rana catesb
4	380	65.6	128	13	Q9DFY8	Q9dfy8 rana catesb
5	305	52.7	128	13	Q9DFY7	Q9dfy7 rana catesb
6	303	52.3	128	13	Q9DFY5	Q9dfy5 rana catesb
7	292	50.4	133	13	Q98SM0	Q98sm0 rana catesb
8	280	48.4	133	13	Q98SL9	Q98sl9 rana catesb
9	279	48.2	132	13	Q98SM2	Q98sm2 rana catesb
10	276	47.7	133	13	Q98SL8	Q98sl8 rana catesb
11	274	47.3	132	13	Q98SM1	Q98sm1 rana catesb
12	269.5	46.5	132	13	Q9DF78	Q9df78 rana catesb
13	153.5	26.5	169	13	Q9W738	Q9w738 xenopus lae
14	122	21.1	157	11	Q9JKJ3	Q9jkj3 meriones un
15	122	21.1	157	11	Q9JKI9	Q9jki9 meriones un
16	120.5	20.8	146	6	Q861Y3	Q861y3 pygathrix r
17	120.5	20.8	146	6	Q861Y2	Q861y2 pygathrix b
18	120.5	20.8	146	6	Q861Y1	Q861y1 pygathrix a
19	120	20.7	152	11	Q9JKI5	Q9jki5 mus saxicol
20	120	20.7	157	11	Q9JKJ4	Q9jkj4 meriones un
21	117.5	20.3	153	11	Q9JKI7	Q9jki7 mus saxicol
22	117	20.2	157	11	Q9JKJ1	Q9jkj1 meriones un
23	117	20.2	157	11	Q9JKJ2	Q9jkj2 meriones un
24	116.5	20.1	146	6	Q861Y4	Q861y4 trachypithe
25	114.5	19.8	132	6	Q9TV24	Q9tv24 galago moho
26	114	19.7	147	6	Q7YRJ5	Q7yrj5 tursiops tr
27	114	19.7	154	11	Q9JKI8	Q9jki8 mus saxicol
28	112	19.3	147	6	Q7YRJ6	Q7yrj6 balaena mys
29	111.5	19.3	155	11	Q9JKH9	Q9jkh9 mus pahari
30	110.5	19.1	119	6	Q9TSQ6	Q9tsq6 cercopithec
31	110.5	19.1	119	6	Q9TV32	Q9tv32 gorilla gor
32	110.5	19.1	132	6	Q9TV25	Q9tv25 eulemur ful
33	110.5	19.1	147	6	Q8HZQ0	Q8hzq0 pan troglod
34	110.5	19.1	155	11	Q9JKI3	Q9jki3 mus saxicol
35	109.5	18.9	119	6	Q9TV30	Q9tv30 saguinus oe
36	109	18.8	146	6	Q861Y5	Q861y5 colobus gue
37	108.5	18.7	155	11	Q9JKH8	Q9jkh8 mus pahari
38	108	18.7	156	11	Q923L6	Q92316 mus musculu
39	107.5	18.6	155	11	Q9JKI6	Q9jki6 mus saxicol
40	107	18.5	124	6	Q95NE6	Q95ne6 bubalus bub
41	106.5	18.4	155	11	Q9JKI2	Q9jki2 mus saxicol
42	106.5	18.4	155	11	Q9R134	Q9r134 rattus norv
43	106.5	18.4	155	11	Q9JKI4	Q9jki4 mus saxicol
44	105.5	18.2	144	11	Q80Z85	Q80z85 mus musculu
45	105.5	18.2	153	11	Q80XS4	Q80xs4 mus musculu

ALIGNMENTS

RESULT 1
Q9I8V8
ID Q9I8V8 PRELIMINARY; PRT; 127 AA.
AC Q9I8V8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Onconase variant rapLR1 precursor.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20330357; PubMed=10871370;
RA Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;
RT "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a
RT 3' UTR of unusual length and structure.";
RL Nucleic Acids Res. 28:2375-2382(2000).
DR EMBL; AF165133; AAF76935.1; -.
DR PIR; A39035; A39035.
DR HSSP; P22069; 1ONC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNAse_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
SQ SEQUENCE 127 AA; 14491 MW; B8511DC5407AB69B CRC64;

Query Match 98.3%; Score 569; DB 13; Length 127;
Best Local Similarity 98.1%; Pred. No. 4.7e-58;
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QDWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 60

; ORGANISM: Rana pipiens
US-09-961-400-2

Query Match 46.8%; Score 281.5; DB 10; Length 104;
Best Local Similarity 49.5%; Pred. No. 2.9e-24;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

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Qy          1 QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 58
              |:| |||:||: ||  : || ||  |::     ||  |||| |    ||||| |:| : |
Db          1 QDWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56

Qy         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
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Search completed: May 7, 2004, 21:51:57
Job time : 35.2947 secs

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;  TITLE OF INVENTION: Recombinant Anti-Tumor RNase
;  FILE REFERENCE: 015280-343110US
;  CURRENT APPLICATION NUMBER: US/09/948,391A
;  CURRENT FILING DATE:  2002-05-10
;  PRIOR APPLICATION NUMBER: US 60/079,751
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: WO PCT/US99/06641
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: US 09/622,613
;  PRIOR FILING DATE: 2000-08-17
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Rana
;   OTHER INFORMATION: catesbeiana ribonuclease with (His)6 tag, Met at
;   OTHER INFORMATION: position 7, Met23Leu and Met58Leu substitutions
;   OTHER INFORMATION: (recombinant Met(-1) RaCOR1 Met22Leu Met57Leu-(His)6)
US-09-948-391A-22

  Query Match             99.0%;  Score 596;  DB 10;  Length 117;
  Best Local Similarity   98.2%;  Pred. No. 4.9e-60;
  Matches  108;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 60
              ||||||||||||||||||||:|||||||||||||||||||||||||||||||||||:|||
Db          8 QNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 67

Qy         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 117


RESULT 13
US-09-961-400-22
; Sequence 22, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
;  APPLICANT: RYBAK, SUSANNA M.
;  APPLICANT:  GOLDENBERG, DAVID M.
;  APPLICANT:  NEWTON, DIANNE L.
;  TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
;  TITLE OF INVENTION:  CELLS
;  FILE REFERENCE: 018733/1059
;  CURRENT APPLICATION NUMBER: US/09/961,400
;  CURRENT FILING DATE:  2001-09-25
;  PRIOR APPLICATION NUMBER: 09/622,613
;  PRIOR FILING DATE: 2000-08-17
;  PRIOR APPLICATION NUMBER: PCT/US99/06641
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: 60/079,751
;  PRIOR FILING DATE: 1998-03-26
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: Rana catesbeiana
US-09-961-400-22

  Query Match             99.0%;  Score 596;  DB 10;  Length 117;
  Best Local Similarity   98.2%;  Pred. No. 4.9e-60;
  Matches  108;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 60
              ||||||||||||||||||||:|||||||||||||||||||||||||||||||||||:|||
Db          8 QNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 67

Qy         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 117


RESULT 14
US-09-948-391A-19
; Sequence 19, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
;  APPLICANT: Rybak, Susanna M.
;  APPLICANT:  Newton, Dianne L.
;  APPLICANT:  The United States of America
;  APPLICANT:  as represented by The Secretary of the
;  APPLICANT:  Department of Health and Human Services
;  TITLE OF INVENTION: Recombinant Anti-Tumor RNase
;  FILE REFERENCE: 015280-343110US
;  CURRENT APPLICATION NUMBER: US/09/948,391A
;  CURRENT FILING DATE:  2002-05-10
;  PRIOR APPLICATION NUMBER: US 60/079,751
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: WO PCT/US99/06641
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: US 09/622,613
;  PRIOR FILING DATE: 2000-08-17
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Rana
;   OTHER INFORMATION: catesbeiana ribonuclease with Met22Leu and
;   OTHER INFORMATION: Met57Leu substitutions (recombinant RaCOR1
;   OTHER INFORMATION: Met22Leu Met57Leu)
US-09-948-391A-19

  Query Match             98.0%;  Score 590;  DB 10;  Length 110;
  Best Local Similarity   97.3%;  Pred. No. 2.2e-59;
  Matches  107;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 60
              |||||||||||| |||||||:|||||||||||||||||||||||||||||||||:|||
Db          1 QNWATFQQKHIIKTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 60

Qy         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110


RESULT 15
US-09-961-400-2
; Sequence 2, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
;  APPLICANT: RYBAK, SUSANNA M.
;  APPLICANT:  GOLDENBERG, DAVID M.
;  APPLICANT:  NEWTON, DIANNE L.
;  TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
;  TITLE OF INVENTION:  CELLS
;  FILE REFERENCE: 018733/1059
;  CURRENT APPLICATION NUMBER: US/09/961,400
;  CURRENT FILING DATE:  2001-09-25
;  PRIOR APPLICATION NUMBER: 09/622,613
;  PRIOR FILING DATE: 2000-08-17
;  PRIOR APPLICATION NUMBER: PCT/US99/06641
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: 60/079,751
;  PRIOR FILING DATE: 1998-03-26
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 104
;   TYPE: PRT
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Qy          61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
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Db          61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110


RESULT 9
US-09-948-391A-17
; Sequence 17, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
;  APPLICANT: Rybak, Susanna M.
;  APPLICANT:  Newton, Dianne L.
;  APPLICANT:  The United States of America
;  APPLICANT:  as represented by The Secretary of the
;  APPLICANT:  Department of Health and Human Services
;  TITLE OF INVENTION: Recombinant Anti-Tumor RNase
;  FILE REFERENCE: 015280-343110US
;  CURRENT APPLICATION NUMBER: US/09/948,391A
;  CURRENT FILING DATE:  2002-05-10
;  PRIOR APPLICATION NUMBER: US 60/079,751
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: WO PCT/US99/06641
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: US 09/622,613
;  PRIOR FILING DATE: 2000-08-17
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
;   LENGTH: 111
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Rana
;   OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1
;   OTHER INFORMATION: (recombinant Met(-1) RaCOR1)
US-09-948-391A-17

  Query Match             99.0%;  Score 596;  DB 10;  Length 111;
  Best Local Similarity   99.1%;  Pred. No. 4.6e-60;
  Matches  109;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db           2 QNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVTTFIISSATTVKAICTGVINMNVL 61

Qy          61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
               ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          62 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111


RESULT 10
US-09-948-391A-21
; Sequence 21, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
;  APPLICANT: Rybak, Susanna M.
;  APPLICANT:  Newton, Dianne L.
;  APPLICANT:  The United States of America
;  APPLICANT:  as represented by The Secretary of the
;  APPLICANT:  Department of Health and Human Services
;  TITLE OF INVENTION: Recombinant Anti-Tumor RNase
;  FILE REFERENCE: 015280-343110US
;  CURRENT APPLICATION NUMBER: US/09/948,391A
;  CURRENT FILING DATE:  2002-05-10
;  PRIOR APPLICATION NUMBER: US 60/079,751
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: WO PCT/US99/06641
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: US 09/622,613
;  PRIOR FILING DATE: 2000-08-17
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
;   LENGTH: 111
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Rana
;   OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1,
;   OTHER INFORMATION: Met23Leu and Met58Leu substitutions (recombinant
;   OTHER INFORMATION: Met(-1) RaCOR1 Met22Leu Met57Leu)
US-09-948-391A-21

  Query Match             99.0%;  Score 596;  DB 10;  Length 111;
  Best Local Similarity   98.2%;  Pred. No. 4.6e-60;
  Matches  108;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 QNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 60
               |||||||||||||||||||:|||||||||||||||||||||||||||||:|||
Db           2 QNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 61

Qy          61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
               ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          62 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111


RESULT 11
US-09-961-400-21
; Sequence 21, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
;  APPLICANT: RYBAK, SUSANNA M.
;  APPLICANT:  GOLDENBERG, DAVID M.
;  APPLICANT:  NEWTON, DIANNE L.
;  TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
;  TITLE OF INVENTION:  CELLS
;  FILE REFERENCE: 018733/1059
;  CURRENT APPLICATION NUMBER: US/09/961,400
;  CURRENT FILING DATE:  2001-09-25
;  PRIOR APPLICATION NUMBER: 09/622,613
;  PRIOR FILING DATE: 2000-08-17
;  PRIOR APPLICATION NUMBER: PCT/US99/06641
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: 60/079,751
;  PRIOR FILING DATE: 1998-03-26
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
;   LENGTH: 111
;   TYPE: PRT
;   ORGANISM: Rana catesbeiana
US-09-961-400-21

  Query Match             99.0%;  Score 596;  DB 10;  Length 111;
  Best Local Similarity   98.2%;  Pred. No. 4.6e-60;
  Matches  108;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 QNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 60
               |||||||||||||||||||:|||||||||||||||||||||||||||||:|||
Db           2 QNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 61

Qy          61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
               ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          62 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111


RESULT 12
US-09-948-391A-22
; Sequence 22, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
;  APPLICANT: Rybak, Susanna M.
;  APPLICANT:  Newton, Dianne L.
;  APPLICANT:  The United States of America
;  APPLICANT:  as represented by The Secretary of the
;  APPLICANT:  Department of Health and Human Services
```

; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-24

Query Match 99.2%; Score 597; DB 10; Length 110;
Best Local Similarity 100.0%; Pred. No. 3.5e-60;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS 61
Db 2 NWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS 61

Qy 62 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db 62 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 6
US-09-948-391A-26
; Sequence 26, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1
; OTHER INFORMATION: and Gln2Ser substitution (Met(-1) RaCOR1 Q1S)
US-09-948-391A-26

Query Match 99.2%; Score 597; DB 10; Length 111;
Best Local Similarity 100.0%; Pred. No. 3.6e-60;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 62 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db 63 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 7
US-09-961-400-26
; Sequence 26, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-26

Query Match 99.2%; Score 597; DB 10; Length 111;
Best Local Similarity 100.0%; Pred. No. 3.6e-60;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS 61
Db 3 NWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS 62

Qy 62 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db 63 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 8
US-09-961-400-19
; Sequence 19, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-19

Query Match 99.0%; Score 596; DB 10; Length 110;
Best Local Similarity 98.2%; Pred. No. 4.6e-60;
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Db         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110


RESULT 2
US-09-961-400-15
; Sequence 15, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
;  APPLICANT: RYBAK, SUSANNA M.
;  APPLICANT:  GOLDENBERG, DAVID M.
;  APPLICANT:  NEWTON, DIANNE L.
;  TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
;  TITLE OF INVENTION:  CELLS
;  FILE REFERENCE: 018733/1059
;  CURRENT APPLICATION NUMBER: US/09/961,400
;  CURRENT FILING DATE:  2001-09-25
;  PRIOR APPLICATION NUMBER: 09/622,613
;  PRIOR FILING DATE: 2000-08-17
;  PRIOR APPLICATION NUMBER: PCT/US99/06641
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: 60/079,751
;  PRIOR FILING DATE: 1998-03-26
;  NUMBER OF SEQ ID NOS: 43
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;   LENGTH: 110
;   TYPE: PRT
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US-09-961-400-15

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RESULT 3
US-09-961-400-17
; Sequence 17, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
;  APPLICANT: RYBAK, SUSANNA M.
;  APPLICANT:  GOLDENBERG, DAVID M.
;  APPLICANT:  NEWTON, DIANNE L.
;  TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
;  TITLE OF INVENTION:  CELLS
;  FILE REFERENCE: 018733/1059
;  CURRENT APPLICATION NUMBER: US/09/961,400
;  CURRENT FILING DATE:  2001-09-25
;  PRIOR APPLICATION NUMBER: 09/622,613
;  PRIOR FILING DATE: 2000-08-17
;  PRIOR APPLICATION NUMBER: PCT/US99/06641
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: 60/079,751
;  PRIOR FILING DATE: 1998-03-26
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.1
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;   ORGANISM: Rana catesbeiana
US-09-961-400-17

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Db         62 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111


RESULT 4
US-09-948-391A-24
; Sequence 24, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
;  APPLICANT: Rybak, Susanna M.
;  APPLICANT:  Newton, Dianne L.
;  APPLICANT:  The United States of America
;  APPLICANT:  as represented by The Secretary of the
;  APPLICANT:  Department of Health and Human Services
;  TITLE OF INVENTION: Recombinant Anti-Tumor RNase
;  FILE REFERENCE: 015280-343110US
;  CURRENT APPLICATION NUMBER: US/09/948,391A
;  CURRENT FILING DATE:  2002-05-10
;  PRIOR APPLICATION NUMBER: US 60/079,751
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: WO PCT/US99/06641
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: US 09/622,613
;  PRIOR FILING DATE: 2000-08-17
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Rana
;   OTHER INFORMATION: catesbeiana ribonuclease with Gln1Ser substitution
;   OTHER INFORMATION: (recombinant RaCOR1 Q1S)
US-09-948-391A-24

  Query Match             99.2%;  Score 597;  DB 10;  Length 110;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-60;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 5
US-09-961-400-24
; Sequence 24, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
;  APPLICANT: RYBAK, SUSANNA M.
;  APPLICANT:  GOLDENBERG, DAVID M.
;  APPLICANT:  NEWTON, DIANNE L.
;  TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
;  TITLE OF INVENTION:  CELLS
;  FILE REFERENCE: 018733/1059
;  CURRENT APPLICATION NUMBER: US/09/961,400
;  CURRENT FILING DATE:  2001-09-25
;  PRIOR APPLICATION NUMBER: 09/622,613
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GenCore version 5.1.6

OM protein - protein search, using sw model

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Title: US-09-961-400-15
Perfect score: 602
Sequence: 1 QNWATFQQKHIINTPIICNT.....ICVKCENQYPVHFAGIGRCP 110

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Gapop 10.0 , Gapext 0.5

Searched: 1140673 seqs, 277566755 residues

Total number of hits satisfying chosen parameters: 1140673

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	602	100.0	110	10	US-09-948-391A-15	Sequence 15, Appl
2	602	100.0	110	10	US-09-961-400-15	Sequence 15, Appl
3	602	100.0	111	10	US-09-961-400-17	Sequence 17, Appl
4	597	99.2	110	10	US-09-948-391A-24	Sequence 24, Appl
5	597	99.2	110	10	US-09-961-400-24	Sequence 24, Appl
6	597	99.2	111	10	US-09-948-391A-26	Sequence 26, Appl
7	597	99.2	111	10	US-09-961-400-26	Sequence 26, Appl
8	596	99.0	110	10	US-09-961-400-19	Sequence 19, Appl
9	596	99.0	111	10	US-09-948-391A-17	Sequence 17, Appl
10	596	99.0	111	10	US-09-948-391A-21	Sequence 21, Appl
11	596	99.0	111	10	US-09-961-400-21	Sequence 21, Appl
12	596	99.0	117	10	US-09-948-391A-22	Sequence 22, Appl
13	596	99.0	117	10	US-09-961-400-22	Sequence 22, Appl
14	590	98.0	110	10	US-09-948-391A-19	Sequence 19, Appl
15	281.5	46.8	104	10	US-09-961-400-2	Sequence 2, Appli
16	281.5	46.8	105	10	US-09-948-391A-6	Sequence 6, Appli
17	281.5	46.8	105	10	US-09-961-400-6	Sequence 6, Appli
18	281.5	46.8	127	10	US-09-948-391A-28	Sequence 28, Appl
19	281.5	46.8	127	10	US-09-961-400-28	Sequence 28, Appl
20	280.5	46.6	104	10	US-09-948-391A-2	Sequence 2, Appli
21	278.5	46.3	111	10	US-09-961-400-9	Sequence 9, Appli
22	277.5	46.1	105	14	US-10-153-882-2	Sequence 2, Appli
23	276.5	45.9	104	10	US-09-948-391A-11	Sequence 11, Appl
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25	276.5	45.9	105	10	US-09-948-391A-13	Sequence 13, Appl
26	276.5	45.9	105	10	US-09-961-400-13	Sequence 13, Appl
27	275.5	45.8	104	10	US-09-948-391A-4	Sequence 4, Appli
28	275.5	45.8	104	10	US-09-961-400-4	Sequence 4, Appli
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34	266.5	44.3	111	10	US-09-948-391A-9	Sequence 9, Appli
35	206	34.2	83	9	US-09-986-119-3	Sequence 3, Appli
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38	135.5	22.5	124	12	US-10-037-417-103	Sequence 103, App
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42	117.5	19.5	124	12	US-10-461-713-52	Sequence 52, Appl
43	117	19.4	147	9	US-09-731-872-254	Sequence 254, App
44	117	19.4	147	10	US-09-876-997-254	Sequence 254, App
45	114.5	19.0	124	9	US-09-981-286A-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-948-391A-15
; Sequence 15, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana oocyte ribonuclease (RaCOR1) synthetic
; OTHER INFORMATION: gene modified to use E. coli preferred codons
US-09-948-391A-15

Query Match 100.0%; Score 602; DB 10; Length 110;
Best Local Similarity 100.0%; Pred. No. 9.5e-61;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; ORGANISM: Rana pipiens
US-09-961-400-9

Query Match 46.6%; Score 279.5; DB 10; Length 111;
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; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1
; OTHER INFORMATION: and Gln2Ser substitution (Met(-1) RaCOR1 Q1S)
US-09-948-391A-26

  Query Match             98.5%;  Score 591;  DB 10;  Length 111;
  Best Local Similarity   98.2%;  Pred. No. 3.9e-59;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 13
US-09-961-400-26
; Sequence 26, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-26

  Query Match             98.5%;  Score 591;  DB 10;  Length 111;
  Best Local Similarity   98.2%;  Pred. No. 3.9e-59;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 NWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVLS 61
              ||||||||||||||||||||:||||||||||||||||||||||||||||||||:||||
Db          3 NWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS 62

Qy         62 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111


RESULT 14
US-09-948-391A-17
; Sequence 17, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1
; OTHER INFORMATION: (recombinant Met(-1) RaCOR1)
US-09-948-391A-17

  Query Match             98.3%;  Score 590;  DB 10;  Length 111;
  Best Local Similarity   97.3%;  Pred. No. 5e-59;
  Matches  107;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 60
              |||||||||||||||||||:||||||||||||||||:|||||||||||||||||||:|||
Db          2 QNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVTTFIISSATTVKAICTGVINMNVL 61

Qy         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111


RESULT 15
US-09-961-400-9
; Sequence 9, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 111
; TYPE: PRT
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Db          2 QNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 61

Qy         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111


RESULT 9
US-09-948-391A-19
; Sequence 19, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
;  APPLICANT: Rybak, Susanna M.
;  APPLICANT:  Newton, Dianne L.
;  APPLICANT:  The United States of America
;  APPLICANT:  as represented by The Secretary of the
;  APPLICANT:  Department of Health and Human Services
;  TITLE OF INVENTION: Recombinant Anti-Tumor RNase
;  FILE REFERENCE: 015280-343110US
;  CURRENT APPLICATION NUMBER: US/09/948,391A
;  CURRENT FILING DATE:  2002-05-10
;  PRIOR APPLICATION NUMBER: US 60/079,751
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: WO PCT/US99/06641
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: US 09/622,613
;  PRIOR FILING DATE: 2000-08-17
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Rana
;   OTHER INFORMATION: catesbeiana ribonuclease with Met22Leu and
;   OTHER INFORMATION: Met57Leu substitutions (recombinant RaCOR1
;   OTHER INFORMATION: Met22Leu Met57Leu)
US-09-948-391A-19

  Query Match             99.0%;  Score 594;  DB 10;  Length 110;
  Best Local Similarity   99.1%;  Pred. No. 1.7e-59;
  Matches  109;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 60
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QNWATFQQKHIIKTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 60

Qy         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110


RESULT 10
US-09-948-391A-24
; Sequence 24, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
;  APPLICANT: Rybak, Susanna M.
;  APPLICANT:  Newton, Dianne L.
;  APPLICANT:  The United States of America
;  APPLICANT:  as represented by The Secretary of the
;  APPLICANT:  Department of Health and Human Services
;  TITLE OF INVENTION: Recombinant Anti-Tumor RNase
;  FILE REFERENCE: 015280-343110US
;  CURRENT APPLICATION NUMBER: US/09/948,391A
;  CURRENT FILING DATE:  2002-05-10
;  PRIOR APPLICATION NUMBER: US 60/079,751
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: WO PCT/US99/06641
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: US 09/622,613
;  PRIOR FILING DATE: 2000-08-17
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Rana
;   OTHER INFORMATION: catesbeiana ribonuclease with Gln1Ser substitution
;   OTHER INFORMATION: (recombinant RaCOR1 Q1S)
US-09-948-391A-24

  Query Match             98.5%;  Score 591;  DB 10;  Length 110;
  Best Local Similarity   98.2%;  Pred. No. 3.8e-59;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 NWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVLS 61
              |||||||||||||||||||:|||||||||||||||||||||||||||||||:||||
Db          2 NWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS 61

Qy         62 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110


RESULT 11
US-09-961-400-24
; Sequence 24, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
;  APPLICANT: RYBAK, SUSANNA M.
;  APPLICANT:  GOLDENBERG, DAVID M.
;  APPLICANT:  NEWTON, DIANNE L.
;  TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
;  TITLE OF INVENTION:  CELLS
;  FILE REFERENCE: 018733/1059
;  CURRENT APPLICATION NUMBER: US/09/961,400
;  CURRENT FILING DATE:  2001-09-25
;  PRIOR APPLICATION NUMBER: 09/622,613
;  PRIOR FILING DATE: 2000-08-17
;  PRIOR APPLICATION NUMBER: PCT/US99/06641
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: 60/079,751
;  PRIOR FILING DATE: 1998-03-26
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: Rana catesbeiana
US-09-961-400-24

  Query Match             98.5%;  Score 591;  DB 10;  Length 110;
  Best Local Similarity   98.2%;  Pred. No. 3.8e-59;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 NWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVLS 61
              |||||||||||||||||||:|||||||||||||||||||||||||||||||:||||
Db          2 NWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS 61

Qy         62 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110


RESULT 12
US-09-948-391A-26
; Sequence 26, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
;  APPLICANT: Rybak, Susanna M.
;  APPLICANT:  Newton, Dianne L.
;  APPLICANT:  The United States of America
```

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;  CURRENT FILING DATE:  2001-09-25
;  PRIOR APPLICATION NUMBER: 09/622,613
;  PRIOR FILING DATE: 2000-08-17
;  PRIOR APPLICATION NUMBER: PCT/US99/06641
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: 60/079,751
;  PRIOR FILING DATE: 1998-03-26
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: Rana catesbeiana
US-09-961-400-22

  Query Match             100.0%;  Score 600;  DB 10;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-60;
  Matches  110;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 QNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 67

Qy         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 117


RESULT 6
US-09-948-391A-15
; Sequence 15, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
;  APPLICANT: Rybak, Susanna M.
;  APPLICANT:  Newton, Dianne L.
;  APPLICANT:  The United States of America
;  APPLICANT:  as represented by The Secretary of the
;  APPLICANT:  Department of Health and Human Services
;  TITLE OF INVENTION: Recombinant Anti-Tumor RNase
;  FILE REFERENCE: 015280-343110US
;  CURRENT APPLICATION NUMBER: US/09/948,391A
;  CURRENT FILING DATE:  2002-05-10
;  PRIOR APPLICATION NUMBER: US 60/079,751
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: WO PCT/US99/06641
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: US 09/622,613
;  PRIOR FILING DATE: 2000-08-17
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Rana
;   OTHER INFORMATION: catesbeiana oocyte ribonuclease (RaCOR1) synthetic
;   OTHER INFORMATION: gene modified to use E. coli preferred codons
US-09-948-391A-15

  Query Match             99.3%;  Score 596;  DB 10;  Length 110;
  Best Local Similarity   98.2%;  Pred. No. 1e-59;
  Matches  108;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 60
              |||||||||||||||||||:|||||||||||||||||||||||||||||:|||
Db          1 QNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 60

Qy         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110


RESULT 7
US-09-961-400-15
; Sequence 15, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
;  APPLICANT: RYBAK, SUSANNA M.
;  APPLICANT:  GOLDENBERG, DAVID M.
;  APPLICANT:  NEWTON, DIANNE L.
;  TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
;  TITLE OF INVENTION:  CELLS
;  FILE REFERENCE: 018733/1059
;  CURRENT APPLICATION NUMBER: US/09/961,400
;  CURRENT FILING DATE:  2001-09-25
;  PRIOR APPLICATION NUMBER: 09/622,613
;  PRIOR FILING DATE: 2000-08-17
;  PRIOR APPLICATION NUMBER: PCT/US99/06641
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: 60/079,751
;  PRIOR FILING DATE: 1998-03-26
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: Rana catesbeiana
US-09-961-400-15

  Query Match             99.3%;  Score 596;  DB 10;  Length 110;
  Best Local Similarity   98.2%;  Pred. No. 1e-59;
  Matches  108;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 60
              |||||||||||||||||||:|||||||||||||||||||||||||||||:|||
Db          1 QNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 60

Qy         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110


RESULT 8
US-09-961-400-17
; Sequence 17, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
;  APPLICANT: RYBAK, SUSANNA M.
;  APPLICANT:  GOLDENBERG, DAVID M.
;  APPLICANT:  NEWTON, DIANNE L.
;  TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
;  TITLE OF INVENTION:  CELLS
;  FILE REFERENCE: 018733/1059
;  CURRENT APPLICATION NUMBER: US/09/961,400
;  CURRENT FILING DATE:  2001-09-25
;  PRIOR APPLICATION NUMBER: 09/622,613
;  PRIOR FILING DATE: 2000-08-17
;  PRIOR APPLICATION NUMBER: PCT/US99/06641
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: 60/079,751
;  PRIOR FILING DATE: 1998-03-26
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
;   LENGTH: 111
;   TYPE: PRT
;   ORGANISM: Rana catesbeiana
US-09-961-400-17

  Query Match             99.3%;  Score 596;  DB 10;  Length 111;
  Best Local Similarity   98.2%;  Pred. No. 1e-59;
  Matches  108;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 60
              |||||||||||||||||||:|||||||||||||||||||||||||||||:|||
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RESULT 2
US-09-948-391A-21
; Sequence 21, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
;  APPLICANT: Rybak, Susanna M.
;  APPLICANT:  Newton, Dianne L.
;  APPLICANT:  The United States of America
;  APPLICANT:  as represented by The Secretary of the
;  APPLICANT:  Department of Health and Human Services
;  TITLE OF INVENTION: Recombinant Anti-Tumor RNase
;  FILE REFERENCE: 015280-343110US
;  CURRENT APPLICATION NUMBER: US/09/948,391A
;  CURRENT FILING DATE:  2002-05-10
;  PRIOR APPLICATION NUMBER: US 60/079,751
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: WO PCT/US99/06641
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: US 09/622,613
;  PRIOR FILING DATE: 2000-08-17
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
;   LENGTH: 111
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Rana
;   OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1,
;   OTHER INFORMATION: Met23Leu and Met58Leu substitutions (recombinant
;   OTHER INFORMATION: Met(-1) RaCOR1 Met22Leu Met57Leu)
US-09-948-391A-21

  Query Match           100.0%;  Score 600;  DB 10;  Length 111;
  Best Local Similarity  100.0%;  Pred. No. 3.7e-60;
  Matches  110;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 QNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 61

Qy         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111


RESULT 3
US-09-961-400-21
; Sequence 21, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
;  APPLICANT: RYBAK, SUSANNA M.
;  APPLICANT:  GOLDENBERG, DAVID M.
;  APPLICANT:  NEWTON, DIANNE L.
;  TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
;  TITLE OF INVENTION:  CELLS
;  FILE REFERENCE: 018733/1059
;  CURRENT APPLICATION NUMBER: US/09/961,400
;  CURRENT FILING DATE:  2001-09-25
;  PRIOR APPLICATION NUMBER: 09/622,613
;  PRIOR FILING DATE: 2000-08-17
;  PRIOR APPLICATION NUMBER: PCT/US99/06641
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: 60/079,751
;  PRIOR FILING DATE: 1998-03-26
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
;   LENGTH: 111
;   TYPE: PRT
;   ORGANISM: Rana catesbeiana
US-09-961-400-21

  Query Match           100.0%;  Score 600;  DB 10;  Length 111;
  Best Local Similarity  100.0%;  Pred. No. 3.7e-60;
  Matches  110;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 QNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 61

Qy         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111


RESULT 4
US-09-948-391A-22
; Sequence 22, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
;  APPLICANT: Rybak, Susanna M.
;  APPLICANT:  Newton, Dianne L.
;  APPLICANT:  The United States of America
;  APPLICANT:  as represented by The Secretary of the
;  APPLICANT:  Department of Health and Human Services
;  TITLE OF INVENTION: Recombinant Anti-Tumor RNase
;  FILE REFERENCE: 015280-343110US
;  CURRENT APPLICATION NUMBER: US/09/948,391A
;  CURRENT FILING DATE:  2002-05-10
;  PRIOR APPLICATION NUMBER: US 60/079,751
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: WO PCT/US99/06641
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: US 09/622,613
;  PRIOR FILING DATE: 2000-08-17
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Rana
;   OTHER INFORMATION: catesbeiana ribonuclease with (His)6 tag, Met at
;   OTHER INFORMATION: position 7, Met23Leu and Met58Leu substitutions
;   OTHER INFORMATION: (recombinant Met(-1) RaCOR1 Met22Leu Met57Leu-(His)6)
US-09-948-391A-22

  Query Match           100.0%;  Score 600;  DB 10;  Length 117;
  Best Local Similarity  100.0%;  Pred. No. 3.9e-60;
  Matches  110;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          8 QNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 67

Qy         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 117


RESULT 5
US-09-961-400-22
; Sequence 22, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
;  APPLICANT: RYBAK, SUSANNA M.
;  APPLICANT:  GOLDENBERG, DAVID M.
;  APPLICANT:  NEWTON, DIANNE L.
;  TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
;  TITLE OF INVENTION:  CELLS
;  FILE REFERENCE: 018733/1059
;  CURRENT APPLICATION NUMBER: US/09/961,400
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:40 ; Search time 35.2947 Seconds
(without alignments)
865.070 Million cell updates/sec

Title: US-09-961-400-19
Perfect score: 600
Sequence: 1 QNWATFQQKHIINTPIICNT.....ICVKCENQYPVHFAGIGRCP 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1140673 seqs, 277566755 residues

Total number of hits satisfying chosen parameters: 1140673

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	600	100.0	110	10	US-09-961-400-19	Sequence 19, Appl
2	600	100.0	111	10	US-09-948-391A-21	Sequence 21, Appl
3	600	100.0	111	10	US-09-961-400-21	Sequence 21, Appl
4	600	100.0	117	10	US-09-948-391A-22	Sequence 22, Appl
5	600	100.0	117	10	US-09-961-400-22	Sequence 22, Appl
6	596	99.3	110	10	US-09-948-391A-15	Sequence 15, Appl
7	596	99.3	110	10	US-09-961-400-15	Sequence 15, Appl
8	596	99.3	111	10	US-09-961-400-17	Sequence 17, Appl
9	594	99.0	110	10	US-09-948-391A-19	Sequence 19, Appl
10	591	98.5	110	10	US-09-948-391A-24	Sequence 24, Appl
11	591	98.5	110	10	US-09-961-400-24	Sequence 24, Appl
12	591	98.5	111	10	US-09-948-391A-26	Sequence 26, Appl
13	591	98.5	111	10	US-09-961-400-26	Sequence 26, Appl
14	590	98.3	111	10	US-09-948-391A-17	Sequence 17, Appl
15	279.5	46.6	111	10	US-09-961-400-9	Sequence 9, Appli
16	277.5	46.2	104	10	US-09-961-400-2	Sequence 2, Appli
17	277.5	46.2	105	10	US-09-948-391A-6	Sequence 6, Appli
18	277.5	46.2	105	10	US-09-961-400-6	Sequence 6, Appli
19	277.5	46.2	127	10	US-09-948-391A-28	Sequence 28, Appl
20	277.5	46.2	127	10	US-09-961-400-28	Sequence 28, Appl
21	276.5	46.1	104	10	US-09-948-391A-2	Sequence 2, Appli
22	276.5	46.1	104	10	US-09-948-391A-4	Sequence 4, Appli
23	276.5	46.1	104	10	US-09-961-400-4	Sequence 4, Appli
24	276.5	46.1	105	10	US-09-961-400-8	Sequence 8, Appli
25	273.5	45.6	105	14	US-10-153-882-2	Sequence 2, Appli
26	272.5	45.4	104	10	US-09-948-391A-11	Sequence 11, Appl
27	272.5	45.4	104	10	US-09-961-400-11	Sequence 11, Appl
28	272.5	45.4	105	10	US-09-948-391A-13	Sequence 13, Appl
29	272.5	45.4	105	10	US-09-961-400-13	Sequence 13, Appl
30	268.5	44.8	104	9	US-09-986-119-1	Sequence 1, Appli
31	268.5	44.8	104	10	US-09-918-887-1	Sequence 1, Appli
32	267.5	44.6	105	10	US-09-948-391A-8	Sequence 8, Appli
33	267.5	44.6	111	10	US-09-948-391A-9	Sequence 9, Appli
34	265.5	44.2	104	12	US-10-461-713-53	Sequence 53, Appl
35	202	33.7	83	9	US-09-986-119-3	Sequence 3, Appli
36	202	33.7	83	10	US-09-918-887-3	Sequence 3, Appli
37	161	26.8	169	13	US-10-016-447-2	Sequence 2, Appli
38	131.5	21.9	124	12	US-10-037-417-103	Sequence 103, App
39	127.5	21.2	119	12	US-10-016-248-89	Sequence 89, Appl
40	127.5	21.2	119	15	US-10-074-978A-139	Sequence 139, App
41	118	19.7	99	15	US-10-074-978A-141	Sequence 141, App
42	117	19.5	147	9	US-09-731-872-254	Sequence 254, App
43	117	19.5	147	10	US-09-876-997-254	Sequence 254, App
44	114	19.0	123	12	US-10-461-713-58	Sequence 58, Appl
45	114	19.0	124	13	US-10-016-447-5	Sequence 5, Appli

ALIGNMENTS

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RESULT 1
US-09-961-400-19
; Sequence 19, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
;  APPLICANT: RYBAK, SUSANNA M.
;  APPLICANT:  GOLDENBERG, DAVID M.
;  APPLICANT:  NEWTON, DIANNE L.
;  TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
;  TITLE OF INVENTION:  CELLS
;  FILE REFERENCE: 018733/1059
;  CURRENT APPLICATION NUMBER: US/09/961,400
;  CURRENT FILING DATE:  2001-09-25
;  PRIOR APPLICATION NUMBER: 09/622,613
;  PRIOR FILING DATE: 2000-08-17
;  PRIOR APPLICATION NUMBER: PCT/US99/06641
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: 60/079,751
;  PRIOR FILING DATE: 1998-03-26
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: Rana catesbeiana
US-09-961-400-19

  Query Match           100.0%;  Score 600;  DB 10;  Length 110;
  Best Local Similarity  100.0%;  Pred. No. 3.7e-60;
  Matches  110;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 60

Qy         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
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Db         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
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ID   Q9BEC1      PRELIMINARY;      PRT;   170 AA.
AC   Q9BEC1;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Brain-type ribonuclease ribonuclease precursor (Fragment).
GN   RNASE B.
OS   Tragulus javanicus (Lesser Malay chevrotain).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Tragulina;
OC   Tragulidae; Tragulus.
OX   NCBI_TaxID=9849;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21347458; PubMed=11453981;
RA   Breukelman H.J., Jekel P.A., Dubois J.Y., Mulder P.P.M.F.A.,
RA   Warmels H.W., Beintema J.J.;
RT   "Secretory ribonucleases in the primitive ruminant chevrotain
RT   (Tragulus javanicus).";
RL   Eur. J. Biochem. 268:3890-3897(2001).
CC   -!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR   EMBL; AJ271299; CAC24723.1; -.
DR   HSSP; P00656; 1LSQ.
DR   GO; GO:0004519; F:endonuclease activity; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Endonuclease; Hydrolase; Nuclease; Signal.
FT   NON_TER       1      1
FT   SIGNAL        <1     19       POTENTIAL.
FT   CHAIN         20     170      BRAIN-TYPE RIBONUCLEASE RIBONUCLEASE.
SQ   SEQUENCE   170 AA;  18832 MW;  AB6CE7E1E5549AA0 CRC64;

  Query Match             21.8%;  Score 131;  DB 6;  Length 170;
  Best Local Similarity   33.1%;  Pred. No. 2.8e-07;
  Matches   41;  Conservative   17;  Mismatches   46;  Indels   20;  Gaps    7;

Qy          4 ATFQQKHI------INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICT----- 52
              | |:::|:      ||:   || :|     :  |:|| |||||  |   |||||:
Db         25 AKFRRQHLDAGNSSINSN-YCNLMMKRR-KMTHGRCKPVNTFIHESLEDVKAICSEKNIT 82

Qy         53 ---GVINMNVLSTTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCEN--QYPVHFAGI 106
                 |  | :  ::|    :  | :|  :  | | | :  :  || | ||     |||| |
Db         83 CKNGQPNCHQSNST-MNITDCRQTGGSKYPNCAYKTSQKQKYIIVACEGTPSVPVHFDGS 141

Qy        107 GRCP 110
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Db        142 AVLP 145


RESULT 15
Q80Z85
ID   Q80Z85      PRELIMINARY;      PRT;   144 AA.
AC   Q80Z85;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Angiogenin-4.
GN   ANG4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NMRI;
RX   MEDLINE=22493143; PubMed=12548285;
RA   Hooper L.V., Stappenbeck T.S., Hong C.V., Gordon J.I.;
RT   "Angiogenins: a new class of microbicidal proteins involved in innate
RT   immunity.";
RL   Nat. Immunol. 4:269-273(2003).
DR   EMBL; AY219870; AAO62354.1; -.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
SQ   SEQUENCE   144 AA;  16554 MW;  09808807C00224C1 CRC64;

  Query Match             21.3%;  Score 128.5;  DB 11;  Length 144;
  Best Local Similarity   38.2%;  Pred. No. 4.6e-07;
  Matches   29;  Conservative   13;  Mismatches   29;  Indels    5;  Gaps    3;

Qy         33 CKRVNTFIISSATTVKAIC---TGVINMNV-LSTTRFQLNTCTRTSITP-RPCPYSSRTE 87
              || ||||| :   ::|||          |  :| : ||: ||| :  :|  || | :  :
Db         62 CKDVNTFIHGTKKNIRAICGKKGSPYGENFRISNSPFQITTCTHSRGSPWPPCGYRAFKD 121

Qy         88 TNYICVKCENQYPVHF 103
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Db        122 FRYIVIACEDGWPVHF 137


Search completed: May  7, 2004, 21:46:03
Job time : 31.2816 secs
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ID   Q9DFY7       PRELIMINARY;      PRT;   128 AA.
AC   Q9DFY7;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RC-RNase3 ribonuclease precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20512555; PubMed=11058105;
RA   Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT   "Purification and cloning of cytotoxic ribonucleases from Rana
RT   catesbeiana (bullfrog).";
RL   Nucleic Acids Res. 28:4097-4104(2000).
DR   EMBL; AF242554; AAG31440.2; -.
DR   HSSP; P22069; 1ONC.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24    128       RC-RNASE3 RIBONUCLEASE.
SQ   SEQUENCE   128 AA;  14517 MW;  2B14986082E0587D CRC64;

  Query Match             37.6%;  Score 226.5;  DB 13;  Length 128;
  Best Local Similarity   41.1%;  Pred. No. 1.5e-18;
  Matches   46;  Conservative   18;  Mismatches   39;  Indels    9;  Gaps    4;

Qy          1 QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGV-INMN 58
              |:| |||:||: :|  : |:  |   ::     ||: |||| :    |||:|  :  | :
Db         24 QDWETFQKKHLTDTKKVKCDVEMAKALF----DCKKTNTFIYALPGRVKALCKNIRDNTD 79

Qy         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
              |||   | |  | |  :   || |    : || ||: | || |:||||:| ||
Db         80 VLSRDAFLLPQCDRIKL---PCHYKLSSSTNTICITCVNQLPIHFAGVGSCP 128


RESULT 12
Q9DFY5
ID   Q9DFY5       PRELIMINARY;      PRT;   128 AA.
AC   Q9DFY5;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RC-RNase6 ribonuclease precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20512555; PubMed=11058105;
RA   Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT   "Purification and cloning of cytotoxic ribonucleases from Rana
RT   catesbeiana (bullfrog).";
RL   Nucleic Acids Res. 28:4097-4104(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF242556; AAG31442.2; -.
DR   HSSP; P22069; 1ONC.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24    128       RC-RNASE6 RIBONUCLEASE.
SQ   SEQUENCE   128 AA;  14804 MW;  AFEBFD67D266C7C2 CRC64;

  Query Match             36.1%;  Score 217.5;  DB 13;  Length 128;
  Best Local Similarity   39.3%;  Pred. No. 1.7e-17;
  Matches   44;  Conservative   19;  Mismatches   40;  Indels    9;  Gaps    4;

Qy          1 QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGV-INMN 58
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Db         24 QDWDTFQKKHLTDTKKVKCDVEMKKALF----DCKKTNTFIFARPPRVQALCKNIKDNTN 79

Qy         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
              |||   | |  | |  :   || |    || ||: |  : |:||||:|:||
Db         80 VLSRDVFYLPQCNRKKL---PCHYRLDGSTNTICLTCMKELPIHFAGVGKCP 128


RESULT 13
Q9W738
ID   Q9W738       PRELIMINARY;      PRT;   169 AA.
AC   Q9W738;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   FRL2 protein.
GN   FRL2.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96069863; PubMed=7585965;
RA   Kinoshita N., Minshull J., Kirschner M.W.;
RT   "The identification of two novel ligands of the FGF receptor by a
RT   yeast screening method and their activity in Xenopus development.";
RL   Cell 83:621-630(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Kinoshita N., Kirschner M.W.;
RL   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF159166; AAD41901.1; -.
DR   HSSP; P00656; 1LSQ.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
SQ   SEQUENCE   169 AA;  18891 MW;  D969F3E43B3CE1B8 CRC64;

  Query Match             27.1%;  Score 163;  DB 13;  Length 169;
  Best Local Similarity   39.3%;  Pred. No. 5.2e-11;
  Matches   44;  Conservative   10;  Mismatches   50;  Indels    8;  Gaps    6;

Qy          1 QNWATFQQKHII--NTPIICN-TIMDNNIYIVGGQCKRVNTFI-ISSATTVKAICTGVIN 56
              ||   | :|||:        || || | ||       ||  ||||  ::   || :| |::
Db         28 QNINAFMEKHIVKEGAETNCNQTIKDRNIRF-KNNCKFRNTFIHDTNGKKVKEMCAGIVK 86

Qy         57 MN-VLSTTRFQLNTCTRTSITPRP--CPYSSRTETNYICVKCENQYPVHFAG 105
              |:|     |  |      | ||  | |:     |  | : ||| |||||||
Db         87 STFVISKELLPLTDCLLMGRTARPPNCAYNQTRTTGVINITCENNYPVHFAG 138


RESULT 14
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RESULT 8
Q8UVX5
ID   Q8UVX5      PRELIMINARY;      PRT;   127 AA.
AC   Q8UVX5;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Onconase precursor.
GN   RPR.
OS   Rana pipiens (Northern leopard frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8404;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Liao Y.-D., Wang S.-C.;
RT   "Rana pipiens onconase genomic DNA.";
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF332139; AAL54383.1; -.
DR   PIR; A39035; A39035.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL       1     23       POTENTIAL.
SQ   SEQUENCE   127 AA;  14469 MW;  953F90D351CFEEF3 CRC64;

  Query Match             46.1%;  Score 277.5;  DB 13;  Length 127;
  Best Local Similarity   49.5%;  Pred. No. 1.7e-24;
  Matches   55;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          1 QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 58
              |:| |||:||| ||  : |: ||  |::     ||  |||| |    ||||| |:| : |
Db         24 QDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 79

Qy         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         80 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 127


RESULT 9
Q9DFY6
ID   Q9DFY6      PRELIMINARY;      PRT;   129 AA.
AC   Q9DFY6;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RC-RNase4 ribonuclease precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20512555; PubMed=11058105;
RA   Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT   "Purification and cloning of cytotoxic ribonucleases from Rana
RT   catesbeiana (bullfrog).";
RL   Nucleic Acids Res. 28:4097-4104(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF242555; AAG31441.2; -.
DR   PDB; 1KVZ; 28-JUL-02.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL       1     23       POTENTIAL.
FT   CHAIN       24    129       RC-RNASE4 RIBONUCLEASE.
SQ   SEQUENCE   129 AA;  14724 MW;  826A62882B10ABDA CRC64;

  Query Match             40.9%;  Score 246;  DB 13;  Length 129;
  Best Local Similarity   43.4%;  Pred. No. 8e-21;
  Matches   49;  Conservative   24;  Mismatches   30;  Indels   10;  Gaps    5;

Qy          1 QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 58
              |:||||::||: :|  : |: :|  :::     ||  |||| |    |||:| ||| : :
Db         24 QDWATFKKKHLTDTWDVDCDNLMPTSLF----DCKDKNTFIYSLPGPVKALCRGVIFSAD 79

Qy         59 VLSTTRFQLNTCTRTSITPR-PCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
              ||| : | |  |   :: || || |  :  :| ||::||:: |||||:| ||
Db         80 VLSNSEFYLAEC---NVKPRKPCKYKLKKSSNRICIRCEHELPVHFAGVGICP 129


RESULT 10
Q9DFY8
ID   Q9DFY8      PRELIMINARY;      PRT;   128 AA.
AC   Q9DFY8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RC-RNase2 ribonuclease precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20512555; PubMed=11058105;
RA   Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT   "Purification and cloning of cytotoxic ribonucleases from Rana
RT   catesbeiana (bullfrog).";
RL   Nucleic Acids Res. 28:4097-4104(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF242553; AAG31439.1; -.
DR   PDB; 1M58; 09-JAN-03.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL       1     23       POTENTIAL.
FT   CHAIN       24    128       RC-RNASE2 RIBONUCLEASE.
SQ   SEQUENCE   128 AA;  14839 MW;  989719CF52053ECC CRC64;

  Query Match             38.1%;  Score 229.5;  DB 13;  Length 128;
  Best Local Similarity   40.2%;  Pred. No. 6.7e-19;
  Matches   45;  Conservative   20;  Mismatches   38;  Indels    9;  Gaps    4;

Qy          1 QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 58
              ||| |||:||: :|  : |:  |   ::     ||: |||| :    |:|:|  :| : |
Db         24 QNWETFQKKHLTDTRDVKCDAEMKKALF----DCKQKNTFIYARPGRVQALCKNIIVSKN 79

Qy         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
              ||||  | |: | |  :   || |  :  :| ||: |||: ||||  :  ||
Db         80 VLSTDEFYLSDCNRIKL---PCHYKLKKSSNTICITCENKLPVHFVAVEECP 128
```

```
RESULT 5
Q98SM1
ID   Q98SM1      PRELIMINARY;      PRT;   132 AA.
AC   Q98SM1;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RNase A-type ribonuclease rc204 precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21539506; PubMed=11683320;
RA   Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT   "Rapid diversification of RNase A superfamily ribonuclease from the
RT   bullfrog, Rana catesbeiana.";
RL   J. Mol. Evol. 53:31-38(2001).
DR   EMBL; AF351208; AAK30254.1; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     22       POTENTIAL.
SQ   SEQUENCE   132 AA;  14704 MW;  95D61760F729868E CRC64;

  Query Match             74.5%;  Score 448.5;  DB 13;  Length 132;
  Best Local Similarity   78.2%;  Pred. No. 1.9e-44;
  Matches   86;  Conservative    7;  Mismatches   16;  Indels    1;  Gaps    1;

Qy          1 QNWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 59
              |:| ||||||| :|  | |||||| :|||| |||||:|||||| ||||||||||||:| ||
Db         23 QDWPTFQQKHIPSTSSIDCNTIMDKDIYIVRGQCKKVNTFIIYSATTVKAICTGVLNSNV 82

Qy         60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              |||||||    ||| || ||||||| ||| |||||||:||||||||:|
Db         83 LSTTRFQLXXXTRTFITSRPCPYSSTKETNKICVKCENEYPVHFAGIGKC 132


RESULT 6
Q9DF78
ID   Q9DF78      PRELIMINARY;      PRT;   132 AA.
AC   Q9DF78;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RC-RNaseL1 ribonuclease precursor.
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20512555; PubMed=11058105;
RA   Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT   "Purification and cloning of cytotoxic ribonucleases from Rana
RT   catesbeiana (bullfrog).";
RL   Nucleic Acids Res. 28:4097-4104(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RA   Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF288642; AAG30414.2; -.
DR   HSSP; P11916; 1BC4.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     21       POTENTIAL.
FT   CHAIN        22    132       RC-RNASEL1 RIBONUCLEASE.
SQ   SEQUENCE   132 AA;  14625 MW;  D8D9A517452FBE53 CRC64;

  Query Match             62.5%;  Score 376;  DB 13;  Length 132;
  Best Local Similarity   65.8%;  Pred. No. 5.6e-36;
  Matches   73;  Conservative    9;  Mismatches   27;  Indels    2;  Gaps    2;

Qy          1 QNWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 58
              |||| |::||| :|  | |||||| ||||||:|| |||||||  |||||:||  :
Db         22 QNWAKFKEKHITSTSSIDCNTIMDKAIYIVGGKCKERNTFIISSEDNVKAICSGVSPDRK 81

Qy         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              |||| |:|||| | ||||||||    : | |||||| | |||| |||:|
Db         82 ELSTTSFKLNTCIRDSITPRPCPYHPSPDNNKICVKCEKQLPVHFVGIGKC 132


RESULT 7
Q9I8V8
ID   Q9I8V8      PRELIMINARY;      PRT;   127 AA.
AC   Q9I8V8;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Onconase variant rapLR1 precursor.
OS   Rana pipiens (Northern leopard frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8404;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=20330357; PubMed=10871370;
RA   Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;
RT   "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a
RT   3' UTR of unusual length and structure.";
RL   Nucleic Acids Res. 28:2375-2382(2000).
DR   EMBL; AF165133; AAF76935.1; -.
DR   PIR; A39035; A39035.
DR   HSSP; P22069; 1ONC.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal.
FT   SIGNAL        1     23       POTENTIAL.
SQ   SEQUENCE   127 AA;  14491 MW;  B8511DC5407AB69B CRC64;

  Query Match             46.8%;  Score 281.5;  DB 13;  Length 127;
  Best Local Similarity   49.5%;  Pred. No. 5.7e-25;
  Matches   55;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          1 QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 58
              |:| |||:||: ||  : || ||  |::     ||  |||| |    ||||| |:| : |
Db         24 QDWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 79

Qy         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         80 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 127
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Qy          60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
               ||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db          83 LSTTRFQLNTCTRTSITPRPCPYSSRTENNYICVKCENQYPVHFAGIGRCP 133
```

RESULT 2
Q98SM2
ID Q98SM2 PRELIMINARY; PRT; 132 AA.
AC Q98SM2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Liao Y.-D., Tang P.-C., Jeng J.-T.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF351207; AAK30253.1; -.
DR EMBL; AF359578; AAL87036.1; -.
DR HSSP; P11916; 1BC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNAse_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 132 RC-RNASE7.
SQ SEQUENCE 132 AA; 14412 MW; 131A745187978687 CRC64;

Query Match 81.0%; Score 487.5; DB 13; Length 132;
Best Local Similarity 83.6%; Pred. No. 5.5e-49;
Matches 92; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

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Qy           1 QNWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 59
               | || |||||| :|  | ||||||||||||||||||:|||||||||||||||| || | ||
Db          23 QTWAKFQQKHIPSTSSINCNTIMDNNIYIVGGQCKKVNTFIISSATTVKAICNGVTNSNV 82

Qy          60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
               || ||||||:|||||||||||||||: ||| |||||||| |||||||||:|
Db          83 LSPTRFQLDTCTRTSITPRPCPYSSKKETNKICVKCENQLPVHFAGIGKC 132
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RESULT 3
Q98SL9
ID Q98SL9 PRELIMINARY; PRT; 133 AA.
AC Q98SL9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RNase A-type ribonuclease rc212 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351210; AAK30256.1; -.
DR HSSP; P11916; 1BC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNAse_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 22 POTENTIAL.
SQ SEQUENCE 133 AA; 14615 MW; C8785B236B26E54E CRC64;

Query Match 79.5%; Score 478.5; DB 13; Length 133;
Best Local Similarity 78.4%; Pred. No. 6.2e-48;
Matches 87; Conservative 11; Mismatches 12; Indels 1; Gaps 1;

```
Qy           1 QNWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 59
               |||||||||| ||  | |: ||:|::||||||||:||||| ||||||| ||:|| :  |
Db          23 QNWATFQQKHITNTSSINCSNIMNNSLYIVGGQCKKVNTFIASSATTVKGICSGVTDKKV 82

Qy          60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
               ||:|:|||: |||  ||||||||||||||||||||||||||||||:||
Db          83 LSSTKFQLDICTRIFITPRPCPYSSRTETNYICVKCENQYPVHFAGIGQCP 133
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RESULT 4
Q98SL8
ID Q98SL8 PRELIMINARY; PRT; 133 AA.
AC Q98SL8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RNase A-type ribonuclease rc218 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351211; AAK30257.1; -.
DR HSSP; P11916; 1BC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNAse_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 22 POTENTIAL.
SQ SEQUENCE 133 AA; 14590 MW; 8B40B9A94FA5B943 CRC64;

Query Match 78.3%; Score 471.5; DB 13; Length 133;
Best Local Similarity 76.6%; Pred. No. 4.1e-47;
Matches 85; Conservative 13; Mismatches 12; Indels 1; Gaps 1;

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Qy           1 QNWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 59
               |||||||::|| ||  | |: ||:|::||||||||:||||| ||||||| ||:|| :  |
Db          23 QNWATFQEQHITNTSSINCSNIMNNSLYIVGGQCKKVNTFIASSATTVKGICSGVTDKKV 82

Qy          60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
               ||:|:|||: |||  ||||||||||||||||||||||||||||||:||
Db          83 LSSTKFQLDICTRIFITPRPCPYSSRTETNYICVKCENQYPVHFAGIGQCP 133
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:10 ; Search time 31.2816 Seconds
(without alignments)
1109.503 Million cell updates/sec

Title: US-09-961-400-15
Perfect score: 602
Sequence: 1 QNWATFQQKHIINTPIICNT.....ICVKCENQYPVHFAGIGRCP 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	560.5	93.1	133	13	Q98SM0	Q98sm0 rana catesb
2	487.5	81.0	132	13	Q98SM2	Q98sm2 rana catesb
3	478.5	79.5	133	13	Q98SL9	Q98sl9 rana catesb
4	471.5	78.3	133	13	Q98SL8	Q98sl8 rana catesb
5	448.5	74.5	132	13	Q98SM1	Q98sm1 rana catesb
6	376	62.5	132	13	Q9DF78	Q9df78 rana catesb
7	281.5	46.8	127	13	Q9I8V8	Q9i8v8 rana pipien
8	277.5	46.1	127	13	Q8UVX5	Q8uvx5 rana pipien
9	246	40.9	129	13	Q9DFY6	Q9dfy6 rana catesb
10	229.5	38.1	128	13	Q9DFY8	Q9dfy8 rana catesb
11	226.5	37.6	128	13	Q9DFY7	Q9dfy7 rana catesb
12	217.5	36.1	128	13	Q9DFY5	Q9dfy5 rana catesb
13	163	27.1	169	13	Q9W738	Q9w738 xenopus lae
14	131	21.8	170	6	Q9BEC1	Q9bec1 tragulus ja
15	128.5	21.3	144	11	Q80Z85	Q80z85 mus musculu
16	128.5	21.3	153	11	Q80XS4	Q80xs4 mus musculu
17	127.5	21.2	147	6	Q7YRJ6	Q7yrj6 balaena mys
18	126	20.9	150	11	Q8VD94	Q8vd94 berylmys bo
19	125.5	20.8	163	6	Q9BDC2	Q9bdc2 antilocapra
20	124.5	20.7	116	6	Q9TVC0	Q9tvc0 sus scrofa
21	124	20.6	150	11	Q8VD88	Q8vd88 rattus norv
22	122.5	20.3	144	6	Q9BH14	Q9bh14 antilocapra
23	121.5	20.2	147	6	Q7YRJ5	Q7yrj5 tursiops tr
24	121	20.1	146	6	Q861Y5	Q861y5 colobus gue
25	120.5	20.0	149	11	Q8K2T2	Q8k2t2 mus musculu
26	120.5	20.0	149	11	Q8C6G3	Q8c6g3 mus musculu
27	120	19.9	150	11	Q8VD92	Q8vd92 rattus exul
28	119.5	19.9	146	6	Q861Y4	Q861y4 trachypithe
29	118.5	19.7	146	6	Q861Y3	Q861y3 pygathrix r
30	118.5	19.7	146	6	Q861Y2	Q861y2 pygathrix b
31	118.5	19.7	146	6	Q861Y1	Q861y1 pygathrix a
32	116.5	19.4	152	11	Q8VD89	Q8vd89 rattus norv
33	114.5	19.0	124	6	Q95NE6	Q95ne6 bubalus bub
34	112.5	18.7	148	11	Q8C7E4	Q8c7e4 mus musculu
35	112.5	18.7	149	11	Q8VD95	Q8vd95 berylmys bo
36	112	18.6	134	6	Q9BDB9	Q9bdb9 tragulus ja
37	111.5	18.5	152	11	Q8VD84	Q8vd84 rattus tiom
38	111.5	18.5	156	6	Q8SQ05	Q8sq05 lagothrix l
39	111	18.4	148	11	Q8C663	Q8c663 mus musculu
40	110.5	18.4	119	6	Q9TV28	Q9tv28 eulemur ful
41	110.5	18.4	119	6	Q9TV30	Q9tv30 saguinus oe
42	109.5	18.2	142	6	Q9BEC3	Q9bec3 tragulus ja
43	109.5	18.2	156	6	Q8SQ06	Q8sq06 ateles geof
44	109	18.1	124	6	Q9BEC2	Q9bec2 tragulus ja
45	108.5	18.0	156	6	Q8SQ08	Q8sq08 saimiri sci

ALIGNMENTS

RESULT 1
Q98SM0
ID Q98SM0 PRELIMINARY; PRT; 133 AA.
AC Q98SM0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RNase A-type ribonuclease rc208 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351209; AAK30255.1; -.
DR HSSP; P11916; 1BC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNAse_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 22 POTENTIAL.
SQ SEQUENCE 133 AA; 14628 MW; 87FCF122C3499E02 CRC64;

Query Match 93.1%; Score 560.5; DB 13; Length 133;
Best Local Similarity 94.6%; Pred. No. 1.7e-57;
Matches 105; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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Db         23 QNWATFQQKHITNTSSINCNTIMDNNIYIVGGQCKGVNTFIISSATTVKAICTGVINMNV 82
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; TELEPHONE: 718-625-0399
; TELEFAX: 718-625-0399
; TELEX: No. 5529775 Applicable
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Rana pipiens
; DEVELOPMENTAL STAGE: Embryo
US-08-283-971-1

Query Match 45.0%; Score 272.5; DB 1; Length 104;
Best Local Similarity 49.1%; Pred. No. 3.5e-24;
Matches 54; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

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Qy          3 NWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMNV 60
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Db          2 DWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV 57

Qy         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              |:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         58 LTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
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Search completed: May 11, 2004, 14:37:53
Job time : 16.5747 secs

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;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/875,811
;      FILING DATE:  19-FEB-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/02588
;      FILING DATE:  19-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/011,800
;      FILING DATE:  21-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Faris, Susan K.
;      REGISTRATION NUMBER:  41,739
;      REFERENCE/DOCKET NUMBER:  015280-244100US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  51:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  358 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-875-811-51

  Query Match             45.8%;  Score 277.5;  DB 3;  Length 358;
  Best Local Similarity   49.1%;  Pred. No. 4.2e-24;
  Matches   55;  Conservative   15;  Mismatches   33;  Indels    9;  Gaps    4;

Qy          1 MSNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NM 58
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Db          1 MEDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASK 56

Qy         59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              |||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         57 NVLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 105


RESULT 14
US-08-875-811-26
; Sequence 26, Application US/08875811
; Patent No. 6045793
;  GENERAL INFORMATION:
;    APPLICANT:  Rybak, Susanna M.
;    APPLICANT:  Newton, Dianne L.
;    APPLICANT:  Boque, Lluis
;    APPLICANT:  Wlodawer, Alexander
;    TITLE OF INVENTION:  Recombinant Ribonuclease Proteins
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/875,811
;      FILING DATE:  19-FEB-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/02588
;      FILING DATE:  19-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/011,800
;      FILING DATE:  21-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Faris, Susan K.
;      REGISTRATION NUMBER:  41,739
;      REFERENCE/DOCKET NUMBER:  015280-244100US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  26:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  105 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-875-811-26

  Query Match             45.6%;  Score 276.5;  DB 3;  Length 105;
  Best Local Similarity   49.1%;  Pred. No. 1.2e-24;
  Matches   55;  Conservative   15;  Mismatches   33;  Indels    9;  Gaps    4;

Qy          1 MSNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NM 58
              ||:| |||:||| ||  : |: ||  |::     ||  |||  |    |||| |:| :
Db          1 MSDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFTYSRPEPVKAICKGIIASK 56

Qy         59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              |||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         57 NVLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 105


RESULT 15
US-08-283-971-1
; Sequence 1, Application US/08283971
; Patent No. 5529775
;  GENERAL INFORMATION:
;    APPLICANT:  Ardelt Ph.D, Wojciech J.
;    APPLICANT:  Mikulski, Stanislaw M.
;    TITLE OF INVENTION:  PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mark H. Jay, P.C.
;      STREET:  P.O. Box 020083, General Post Office
;      CITY:  Brooklyn
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  11202-0002
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/283,971
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/921,180
;      FILING DATE:  30-JUL-1992
;      APPLICATION NUMBER:  US 07/178,118
;      FILING DATE:  06-APR-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/436,141
;      FILING DATE:  13-NOV-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jay, Mark H.
;      REGISTRATION NUMBER:  27507
;      REFERENCE/DOCKET NUMBER:  5006 US
;    TELECOMMUNICATION INFORMATION:
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Qy          1 MSNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NM 58
              ||:| |||:||| ||  : |: ||  |::     ||  |||| |    ||||| |:| :
Db        262 MSDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASK 317

Qy         59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              |||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db        318 NVLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 366


RESULT 11
US-08-875-811-39
; Sequence 39, Application US/08875811
; Patent No. 6045793
;  GENERAL INFORMATION:
;    APPLICANT:  Rybak, Susanna M.
;    APPLICANT:  Newton, Dianne L.
;    APPLICANT:  Boque, Lluis
;    APPLICANT:  Wlodawer, Alexander
;    TITLE OF INVENTION:  Recombinant Ribonuclease Proteins
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/875,811
;      FILING DATE:  19-FEB-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/02588
;      FILING DATE:  19-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/011,800
;      FILING DATE:  21-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Faris, Susan K.
;      REGISTRATION NUMBER:  41,739
;      REFERENCE/DOCKET NUMBER:  015280-244100US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  39:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  105 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-875-811-39

  Query Match             45.8%;  Score 277.5;  DB 3;  Length 105;
  Best Local Similarity   49.1%;  Pred. No. 9.4e-25;
  Matches   55;  Conservative   15;  Mismatches   33;  Indels    9;  Gaps    4;

Qy          1 MSNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NM 58
              | :| |||:||| ||  : |: ||  |::     ||  |||| |    ||||| |:| :
Db          1 MEDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASK 56

Qy         59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              |||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         57 NVLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 105


RESULT 12
US-08-875-811-41
; Sequence 41, Application US/08875811
; Patent No. 6045793
;  GENERAL INFORMATION:
;    APPLICANT:  Rybak, Susanna M.
;    APPLICANT:  Newton, Dianne L.
;    APPLICANT:  Boque, Lluis
;    APPLICANT:  Wlodawer, Alexander
;    TITLE OF INVENTION:  Recombinant Ribonuclease Proteins
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/875,811
;      FILING DATE:  19-FEB-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/02588
;      FILING DATE:  19-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/011,800
;      FILING DATE:  21-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Faris, Susan K.
;      REGISTRATION NUMBER:  41,739
;      REFERENCE/DOCKET NUMBER:  015280-244100US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  41:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  355 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-875-811-41

  Query Match             45.8%;  Score 277.5;  DB 3;  Length 355;
  Best Local Similarity   49.1%;  Pred. No. 4.1e-24;
  Matches   55;  Conservative   15;  Mismatches   33;  Indels    9;  Gaps    4;

Qy          1 MSNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NM 58
              | :| |||:||| ||  : |: ||  |::     ||  |||| |    ||||| |:| :
Db        251 MEDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASK 306

Qy         59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
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Db        307 NVLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 355


RESULT 13
US-08-875-811-51
; Sequence 51, Application US/08875811
; Patent No. 6045793
;  GENERAL INFORMATION:
;    APPLICANT:  Rybak, Susanna M.
;    APPLICANT:  Newton, Dianne L.
;    APPLICANT:  Boque, Lluis
;    APPLICANT:  Wlodawer, Alexander
;    TITLE OF INVENTION:  Recombinant Ribonuclease Proteins
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
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;      FILING DATE:  21-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Faris, Susan K.
;      REGISTRATION NUMBER:  41,739
;      REFERENCE/DOCKET NUMBER:  015280-244100US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  57:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  355 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-875-811-57

  Query Match             46.5%;  Score 281.5;  DB 3;  Length 355;
  Best Local Similarity   50.0%;  Pred. No. 1.4e-24;
  Matches   56;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          1 MSNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NM 58
              ||:| |||:||| ||  : |: ||  |::     ||  |||| |    ||||| |:| :
Db          1 MSDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASK 56

Qy         59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              |||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         57 NVLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 105


RESULT 9
US-08-875-811-64
; Sequence 64, Application US/08875811
; Patent No. 6045793
;  GENERAL INFORMATION:
;    APPLICANT:  Rybak, Susanna M.
;    APPLICANT:  Newton, Dianne L.
;    APPLICANT:  Boque, Lluis
;    APPLICANT:  Wlodawer, Alexander
;    TITLE OF INVENTION:  Recombinant Ribonuclease Proteins
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/875,811
;      FILING DATE:  19-FEB-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/02588
;      FILING DATE:  19-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/011,800
;      FILING DATE:  21-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Faris, Susan K.
;      REGISTRATION NUMBER:  41,739
;      REFERENCE/DOCKET NUMBER:  015280-244100US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  64:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  355 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  Protein
;      LOCATION:  1..355
;      OTHER INFORMATION:  /note= "E6FB[Met-(-1)]SerrOnc"
US-08-875-811-64

  Query Match             46.5%;  Score 281.5;  DB 3;  Length 355;
  Best Local Similarity   50.0%;  Pred. No. 1.4e-24;
  Matches   56;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          1 MSNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NM 58
              ||:| |||:||| ||  : |: ||  |::     ||  |||| |    ||||| |:| :
Db        251 MSDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASK 306

Qy         59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              |||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db        307 NVLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 355


RESULT 10
US-08-875-811-55
; Sequence 55, Application US/08875811
; Patent No. 6045793
;  GENERAL INFORMATION:
;    APPLICANT:  Rybak, Susanna M.
;    APPLICANT:  Newton, Dianne L.
;    APPLICANT:  Boque, Lluis
;    APPLICANT:  Wlodawer, Alexander
;    TITLE OF INVENTION:  Recombinant Ribonuclease Proteins
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/875,811
;      FILING DATE:  19-FEB-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/02588
;      FILING DATE:  19-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/011,800
;      FILING DATE:  21-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Faris, Susan K.
;      REGISTRATION NUMBER:  41,739
;      REFERENCE/DOCKET NUMBER:  015280-244100US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  55:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  366 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-875-811-55

  Query Match             46.5%;  Score 281.5;  DB 3;  Length 366;
  Best Local Similarity   50.0%;  Pred. No. 1.5e-24;
  Matches   56;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;
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;    APPLICANT:  Wlodawer, Alexander
;    TITLE OF INVENTION:  Recombinant Ribonuclease Proteins
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/875,811
;      FILING DATE:  19-FEB-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/02588
;      FILING DATE:  19-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/011,800
;      FILING DATE:  21-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Faris, Susan K.
;      REGISTRATION NUMBER:  41,739
;      REFERENCE/DOCKET NUMBER:  015280-244100US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  61:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  254 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-875-811-61

  Query Match           46.5%;  Score 281.5;  DB 3;  Length 254;
  Best Local Similarity   50.0%;  Pred. No. 9.5e-25;
  Matches   56;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          1 MSNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NM 58
              ||:| |||:||| ||  : |: ||  |::     ||  |||| |    ||||| |:| :
Db          1 MSDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASK 56

Qy         59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              |||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         57 NVLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 105


RESULT 7
US-08-875-811-49
; Sequence 49, Application US/08875811
; Patent No. 6045793
;  GENERAL INFORMATION:
;    APPLICANT:  Rybak, Susanna M.
;    APPLICANT:  Newton, Dianne L.
;    APPLICANT:  Boque, Lluis
;    APPLICANT:  Wlodawer, Alexander
;    TITLE OF INVENTION:  Recombinant Ribonuclease Proteins
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/875,811
;      FILING DATE:  19-FEB-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/02588
;      FILING DATE:  19-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/011,800
;      FILING DATE:  21-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Faris, Susan K.
;      REGISTRATION NUMBER:  41,739
;      REFERENCE/DOCKET NUMBER:  015280-244100US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  49:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  355 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-875-811-49

  Query Match           46.5%;  Score 281.5;  DB 3;  Length 355;
  Best Local Similarity   50.0%;  Pred. No. 1.4e-24;
  Matches   56;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          1 MSNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NM 58
              ||:| |||:||| ||  : |: ||  |::     ||  |||| |    ||||| |:| :
Db        251 MSDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASK 306

Qy         59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              |||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db        307 NVLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 355


RESULT 8
US-08-875-811-57
; Sequence 57, Application US/08875811
; Patent No. 6045793
;  GENERAL INFORMATION:
;    APPLICANT:  Rybak, Susanna M.
;    APPLICANT:  Newton, Dianne L.
;    APPLICANT:  Boque, Lluis
;    APPLICANT:  Wlodawer, Alexander
;    TITLE OF INVENTION:  Recombinant Ribonuclease Proteins
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/875,811
;      FILING DATE:  19-FEB-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/02588
;      FILING DATE:  19-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/011,800
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;      DEVELOPMENTAL STAGE:  Oocyte
US-08-467-955-2

  Query Match             46.6%;  Score 282.5;  DB 1;  Length 104;
  Best Local Similarity   50.0%;  Pred. No. 2.4e-25;
  Matches   55;  Conservative   15;  Mismatches   31;  Indels    9;  Gaps    4;

Qy          3 NWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMNV 60
              :| |||:||: ||  : || ||  |::     ||  |||| |    |||| |:| : ||
Db          2 DWLTFQKKHVTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV 57

Qy         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              |:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:|||
Db         58 LTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGRC 104


RESULT 4
US-08-875-811-32
; Sequence 32, Application US/08875811
; Patent No. 6045793
;  GENERAL INFORMATION:
;    APPLICANT:  Rybak, Susanna M.
;    APPLICANT:  Newton, Dianne L.
;    APPLICANT:  Boque, Lluis
;    APPLICANT:  Wlodawer, Alexander
;    TITLE OF INVENTION:  Recombinant Ribonuclease Proteins
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/875,811
;      FILING DATE:  19-FEB-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/02588
;      FILING DATE:  19-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/011,800
;      FILING DATE:  21-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Faris, Susan K.
;      REGISTRATION NUMBER:  41,739
;      REFERENCE/DOCKET NUMBER:  015280-244100US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  112 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-875-811-32

  Query Match             46.5%;  Score 281.5;  DB 3;  Length 112;
  Best Local Similarity   50.0%;  Pred. No. 3.5e-25;
  Matches   56;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          1 MSNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NM 58
              ||:| |||:||| ||  : |: ||  |::     ||  |||| |    ||||| |:| :
Db          8 MSDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASK 63

Qy         59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              |||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         64 NVLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 112


RESULT 5
US-08-875-811-59
; Sequence 59, Application US/08875811
; Patent No. 6045793
;  GENERAL INFORMATION:
;    APPLICANT:  Rybak, Susanna M.
;    APPLICANT:  Newton, Dianne L.
;    APPLICANT:  Boque, Lluis
;    APPLICANT:  Wlodawer, Alexander
;    TITLE OF INVENTION:  Recombinant Ribonuclease Proteins
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/875,811
;      FILING DATE:  19-FEB-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/02588
;      FILING DATE:  19-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/011,800
;      FILING DATE:  21-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Faris, Susan K.
;      REGISTRATION NUMBER:  41,739
;      REFERENCE/DOCKET NUMBER:  015280-244100US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  59:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  251 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-875-811-59

  Query Match             46.5%;  Score 281.5;  DB 3;  Length 251;
  Best Local Similarity   50.0%;  Pred. No. 9.3e-25;
  Matches   56;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          1 MSNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NM 58
              ||:| |||:||| ||  : |: ||  |::     ||  |||| |    ||||| |:| :
Db        147 MSDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASK 202

Qy         59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              |||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db        203 NVLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 251


RESULT 6
US-08-875-811-61
; Sequence 61, Application US/08875811
; Patent No. 6045793
;  GENERAL INFORMATION:
;    APPLICANT:  Rybak, Susanna M.
;    APPLICANT:  Newton, Dianne L.
;    APPLICANT:  Boque, Lluis
```

```
;       STRANDEDNESS:
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
;     FEATURE:
;       NAME/KEY:  Protein
;       LOCATION:  1..111
;       OTHER INFORMATION:  /note= "Frog Lectin from Rana
;       OTHER INFORMATION:  catesbeiana"
US-08-891-848-12

  Query Match             96.8%;  Score 586.5;  DB 2;  Length 111;
  Best Local Similarity   99.1%;  Pred. No. 1.9e-60;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          3 NWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 61
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db          2 NWATFQQKHIINTPIINCNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 61

Qy         62 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111


RESULT 2
US-08-875-811-8
; Sequence 8, Application US/08875811
; Patent No. 6045793
;  GENERAL INFORMATION:
;    APPLICANT:  Rybak, Susanna M.
;    APPLICANT:  Newton, Dianne L.
;    APPLICANT:  Boque, Lluis
;    APPLICANT:  Wlodawer, Alexander
;    TITLE OF INVENTION:  Recombinant Ribonuclease Proteins
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/875,811
;      FILING DATE:  19-FEB-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/02588
;      FILING DATE:  19-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/011,800
;      FILING DATE:  21-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Faris, Susan K.
;      REGISTRATION NUMBER:  41,739
;      REFERENCE/DOCKET NUMBER:  015280-244100US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  111 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  Protein
;      LOCATION:  1..111
;      OTHER INFORMATION:  /note= "Frog Lectin from Rana
;      OTHER INFORMATION:  catesbeiana"
US-08-875-811-8

  Query Match             96.8%;  Score 586.5;  DB 3;  Length 111;
  Best Local Similarity   99.1%;  Pred. No. 1.9e-60;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          3 NWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 61
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db          2 NWATFQQKHIINTPIINCNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 61

Qy         62 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111


RESULT 3
US-08-467-955-2
; Sequence 2, Application US/08467955
; Patent No. 5728805
;  GENERAL INFORMATION:
;    APPLICANT:  Ardelt Ph.D, Wojciech J.
;    TITLE OF INVENTION:  PHARMACEUTICALS AND METHOD FOR MAKING THEM
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mark H. Jay, P.A.
;      STREET:  P.O. Box E
;      CITY:  Short Hills
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07078-0383
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/467,955
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/178,118
;      FILING DATE:  06-APR-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/436,141
;      FILING DATE:  13-NOV-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/814,332
;      FILING DATE:  03-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/283,970
;      FILING DATE:  01-AUG-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jay, Mark H.
;      REGISTRATION NUMBER:  27507
;      REFERENCE/DOCKET NUMBER:  5007 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-912-9066
;      TELEFAX:  201-912-0442
;      TELEX:  No. 5728805 Applicable
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  104 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  N
;    ANTI-SENSE:  N
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  Rana pipiens
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 11, 2004, 14:33:03 ; Search time 16.5747 Seconds
(without alignments)
345.738 Million cell updates/sec

Title: US-09-961-400-26
Perfect score: 606
Sequence: 1 MSNWATFQQKHIINTPIICN.....ICVKCENQYPVHFAGIGRCP 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	586.5	96.8	111	2	US-08-891-848-12	Sequence 12, Appl
2	586.5	96.8	111	3	US-08-875-811-8	Sequence 8, Appli
3	282.5	46.6	104	1	US-08-467-955-2	Sequence 2, Appli
4	281.5	46.5	112	3	US-08-875-811-32	Sequence 32, Appl
5	281.5	46.5	251	3	US-08-875-811-59	Sequence 59, Appl
6	281.5	46.5	254	3	US-08-875-811-61	Sequence 61, Appl
7	281.5	46.5	355	3	US-08-875-811-49	Sequence 49, Appl
8	281.5	46.5	355	3	US-08-875-811-57	Sequence 57, Appl
9	281.5	46.5	355	3	US-08-875-811-64	Sequence 64, Appl
10	281.5	46.5	366	3	US-08-875-811-55	Sequence 55, Appl
11	277.5	45.8	105	3	US-08-875-811-39	Sequence 39, Appl
12	277.5	45.8	355	3	US-08-875-811-41	Sequence 41, Appl
13	277.5	45.8	358	3	US-08-875-811-51	Sequence 51, Appl
14	276.5	45.6	105	3	US-08-875-811-26	Sequence 26, Appl
15	272.5	45.0	104	1	US-08-283-971-1	Sequence 1, Appli
16	272.5	45.0	104	1	US-07-921-619-1	Sequence 1, Appli
17	272.5	45.0	104	1	US-08-467-955-1	Sequence 1, Appli
18	272.5	45.0	104	2	US-08-891-848-13	Sequence 13, Appl
19	272.5	45.0	104	3	US-08-875-811-1	Sequence 1, Appli
20	272.5	45.0	104	3	US-09-394-268-1	Sequence 1, Appli
21	272.5	45.0	104	4	US-09-071-672-1	Sequence 1, Appli
22	272.5	45.0	104	4	US-09-687-748-1	Sequence 1, Appli
23	272.5	45.0	104	4	US-08-626-288-1	Sequence 1, Appli
24	272.5	45.0	104	4	US-09-095-429-1	Sequence 1, Appli
25	272.5	45.0	104	4	US-09-986-119-1	Sequence 1, Appli
26	272.5	45.0	106	3	US-08-875-811-28	Sequence 28, Appl
27	272.5	45.0	107	3	US-08-875-811-30	Sequence 30, Appl
28	272.5	45.0	129	3	US-08-875-811-63	Sequence 63, Appl
29	272.5	45.0	358	3	US-08-875-811-45	Sequence 45, Appl
30	272.5	45.0	365	3	US-08-875-811-53	Sequence 53, Appl
31	272.5	45.0	379	3	US-08-875-811-43	Sequence 43, Appl
32	270.5	44.6	105	3	US-08-875-811-24	Sequence 24, Appl
33	269.5	44.5	104	4	US-08-626-288-2	Sequence 2, Appli
34	269.5	44.5	104	4	US-09-095-429-2	Sequence 2, Appli
35	267.5	44.1	104	3	US-09-394-268-2	Sequence 2, Appli
36	267.5	44.1	104	4	US-09-687-748-2	Sequence 2, Appli
37	254.5	42.0	107	3	US-08-875-811-20	Sequence 20, Appl
38	239.5	39.5	111	3	US-08-875-811-22	Sequence 22, Appl
39	236.5	39.0	360	3	US-08-875-811-47	Sequence 47, Appl
40	235	38.8	114	3	US-09-223-118-3	Sequence 3, Appli
41	226	37.3	114	3	US-09-223-118-2	Sequence 2, Appli
42	225	37.1	114	3	US-09-223-118-1	Sequence 1, Appli
43	224	37.0	114	3	US-09-223-118-4	Sequence 4, Appli
44	206	34.0	83	3	US-08-875-811-2	Sequence 2, Appli
45	206	34.0	83	4	US-09-071-672-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-891-848-12
; Sequence 12, Application US/08891848
; Patent No. 5955073
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Youle, Richard J.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Nicholls, Peter J.
; TITLE OF INVENTION: Selective RNase Cytotoxic Reagents
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,848
; FILING DATE: No. 5955073 yet assigned
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/125,462
; FILING DATE: 22-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/014,082
; FILING DATE: 04-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/779,195
; FILING DATE: 22-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/510,696
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-110310US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid

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Qy          34 CKRVNTFIISSATTVKAICTG----VINMNVLSTTRFQLNTCTRTSITPR-PCPYSSRTE 88
               || |||||  :   :||||        |    | : ||: ||     : | || | :
Db          39 CKEVNTFIHGTRNDIKAICNDKNGEPYNNFRRSKSPFQITTCKHKGGSNRPPCGYRATAG 98

Qy          89 TNYICVKCENQYPVHF 104
                 | | |||  ||||
Db          99 FRTIAVACENGLPVHF 114


RESULT 15
NRGPB
pancreatic ribonuclease (EC 3.1.27.5) B - guinea pig (tentative sequence)
N;Alternate names: RNase IB
C;Species: Cavia porcellus (guinea pig)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C;Accession: A00826
R;van den Berg, A.; van den Hende-Timmer, L.; Hofsteenge, J.; Gaastra, W.; Beintema, J.J
Eur. J. Biochem. 75, 91-100, 1977
A;Title: Guinea pig pancreatic ribonucleases. Isolation, properties, primary structure a
A;Reference number: A91247; MUID:77185023; PMID:862624
A;Accession: A00826
A;Molecule type: protein
A;Residues: 1-128 <VAN>
A;Note: 64-Pro was also found
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;21,34/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted

  Query Match             19.6%;  Score 118.5;  DB 1;  Length 128;
  Best Local Similarity   31.6%;  Pred. No. 8.7e-05;
  Matches   37;  Conservative   14;  Mismatches   43;  Indels   23;  Gaps    6;

Qy           7 FQQKHI------INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60
               ||:|:        |:    || :|     :  |:|| ||||:  |    |:|:|      ||
Db           8 FQRQHMDPEGSPSNSSNYCNVMMIRR-NMTQGRCKPVNTFVHESLADVQAVC---FQKNV 63

Qy          61 L----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCENQ--YPVHF 104
               |          | :| ::  |  || :  | | |        | | ||     ||||
Db          64 LCKNGQTNCYQSYSRMRITDCRVTSSSKFPNCSYRMSQAQKSIIVACEGDPYVPVHF 120


Search completed: May 11, 2004, 14:37:08
Job time : 13.5611 secs
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Db         62 NVACKNGQTNCYQSYSTMSITDCRETGSSKYPNCAYKTTQAKKHIIVACEGNPYVPVHY 120


RESULT 11
NRKGR
pancreatic ribonuclease (EC 3.1.27.5) - red kangaroo
N;Alternate names: RNase 1; RNase A
C;Species: Macropus rufus, Megaleia rufa (red kangaroo)
C;Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 04-Oct-1996
C;Accession: A00833
R;Gaastra, W.; Welling, G.W.; Beintema, J.J.
Eur. J. Biochem. 86, 209-217, 1978
A;Title: The amino-acid sequence of kangaroo pancreatic ribonuclease.
A;Reference number: A00833; MUID:78190621; PMID:658039
A;Accession: A00833
A;Molecule type: protein
A;Residues: 1-122 <GAA>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;11,40,117/Active site: His, Lys, His #status predicted
F;25-83,39-94,57-109,64-71/Disulfide bonds: #status predicted
F;61/Binding site: carbohydrate (Asn) (covalent) #status absent

  Query Match             20.1%;  Score 122;  DB 1;  Length 122;
  Best Local Similarity   30.7%;  Pred. No. 3.7e-05;
  Matches   35;  Conservative   16;  Mismatches   45;  Indels   18;  Gaps    6;

Qy          7 FQQKHI------INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAIC-------- 52
              ||::|:       ::   || :|     :  |:|| :||||    : | |:|
Db          7 FQRQHMDTEHSTASSSNYCNLMMKAR-DMTSGRCKPLNTFIHEPKSVVDAVCHQENVTCK 65

Qy         53 TGVINMNVLSTTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCENQY-PVHF 104
               |  |    | :|  :  | :|  :  | | | :      | | || || ||||
Db         66 NGRTNC-YKSNSRLSITNCRQTGASKYPNCQYETSNLNKQIIVACEGQYVPVHF 118


RESULT 12
NRCU
pancreatic ribonuclease (EC 3.1.27.5) - nutria (tentative sequence)
N;Alternate names: RNase 1; RNase A
C;Species: Myocastor coypus (nutria, coypu)
C;Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
C;Accession: A00822
R;van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
Biochim. Biophys. Acta 453, 400-409, 1976
A;Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic
A;Reference number: A90612; MUID:77065676; PMID:999896
A;Accession: A00822
A;Molecule type: protein
A;Residues: 1-128 <VAN>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F;34/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match             19.9%;  Score 120.5;  DB 1;  Length 128;
  Best Local Similarity   31.6%;  Pred. No. 5.5e-05;
  Matches   37;  Conservative   15;  Mismatches   42;  Indels   23;  Gaps    7;

Qy          7 FQQKHI------INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60
              |:::|:          |  || :| :   :  |:|| ||||:       |:|:|       ||
Db          8 FERQHMDSRGSPSTNPNYCNEMMKSR-NMTQGRCKPVNTFVHEPLADVQAVC---FQKNV 63

Qy         61 L----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 104
              |          | :   :  |  || :  | | | :   |   | | || | | ||||
Db         64 LCKNGQTNCYQSNSNMHITDCRVTSNSDYPNCSYRTSQEEKSIVVACEGNPYVPVHF 120


RESULT 13
NRMS
pancreatic ribonuclease (EC 3.1.27.5) precursor - mouse
N;Alternate names: RNase 1; RNase A
C;Species: Mus musculus (house mouse)
C;Date: 30-Nov-1980 #sequence_revision 13-Mar-1997 #text_change 18-Jun-1999
C;Accession: A34090; S22598; A00830
R;Schueller, C.; Nijssen, H.M.J.; Kok, R.; Beintema, J.J.
Mol. Biol. Evol. 7, 29-44, 1990
A;Title: Evolution of nucleic acids coding for ribonucleases: the mRNA sequence of mouse
A;Reference number: A34090; MUID:90136034; PMID:2299980
A;Accession: A34090
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-149 <SCH>
A;Cross-references: GB:M27814; NID:g200762; PIDN:AAA40060.1; PID:g200763
R;Samuelson, L.C.; Wiebauer, K.; Howard, G.; Schmid, R.M.; Koeplin, D.; Meisler, M.H.
Nucleic Acids Res. 19, 6935-6941, 1991
A;Title: Isolation of the murine ribonuclease gene Rib-1: structure and tissue specific e
A;Reference number: S22598; MUID:92107684; PMID:1840677
A;Accession: S22598
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-149 <SAM>
A;Cross-references: EMBL:X60103; NID:g53981; PIDN:CAA42697.1; PID:g53982
R;Lenstra, J.A.; Beintema, J.J.
Eur. J. Biochem. 98, 399-408, 1979
A;Title: The amino acid sequence of mouse pancreatic ribonuclease.
A;Reference number: A00830; MUID:80024269; PMID:556267
A;Accession: A00830
A;Molecule type: protein
A;Residues: 26-149 <LEN>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-149/Product: pancreatic ribonuclease #status experimental <MAT>
F;37,66,144/Active site: His, Lys, His #status predicted
F;51-109,65-120,83-135,90-97/Disulfide bonds: #status predicted
F;62,87/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             19.9%;  Score 120.5;  DB 1;  Length 149;
  Best Local Similarity   30.8%;  Pred. No. 6.5e-05;
  Matches   36;  Conservative   16;  Mismatches   42;  Indels   23;  Gaps    7;

Qy          7 FQQKHI------INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60
              ||::|:       ||:|  || :|     :  | || ||||:      |:|:|:      ||
Db         33 FQRQHMDPDGSSINSPTYCNQMMKRR-DMTNGSCKPVNTFVHEPLADVQAVCS---QENV 88

Qy         61 L----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 104
                        |::   :  |     :  | | | :     :| | || | | ||||
Db         89 TCKNRKSNCYKSSSALHITDCHLKGNSKYPNCDYKTTQYQKHIIVACEGNPYVPVHF 145


RESULT 14
A43825
angiogenin - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S29834; A43825
R;Bond, M.D.; Strydom, D.J.; Vallee, B.L.
Biochim. Biophys. Acta 1162, 177-186, 1993
A;Title: Characterization and sequencing of rabbit, pig and mouse angiogenins: discernmer
A;Reference number: S29833; MUID:93192291; PMID:8448182
A;Accession: S29834
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-123 <BON>
A;Note: this sequence was submitted to the Protein Sequence Database, December 1992
C;Superfamily: pancreatic ribonuclease

  Query Match             19.7%;  Score 119.5;  DB 1;  Length 123;
  Best Local Similarity   39.5%;  Pred. No. 6.7e-05;
  Matches   30;  Conservative    6;  Mismatches   35;  Indels    5;  Gaps    2;
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```
S20066
pancreatic-type ribonuclease (EC 3.1.27.5) BRb precursor, brain - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 22-Nov-1993 #sequence_revision 12-May-1995 #text_change 22-Jun-1999
C;Accession: S20066; JX0056
R;Sasso, M.P.; Carsana, A.; Confalone, E.; Cosi, C.; Sorrentino, S.; Viola, M.; Palmieri
Nucleic Acids Res. 19, 6469-6474, 1991
A;Title: Molecular cloning of the gene encoding the bovine brain ribonuclease and its ex
A;Reference number: S20066; MUID:92093604; PMID:1754384
A;Accession: S20066
A;Molecule type: DNA
A;Residues: 1-167 <SAS>
A;Cross-references: EMBL:X59767; NID:g150; PIDN:CAA42439.1; PID:g151
R;Watanabe, H.; Katoh, H.; Ishii, M.; Komoda, Y.; Sanda, A.; Takizawa, Y.; Ohgi, K.; Iri
J. Biochem. 104, 939-945, 1988
A;Title: Primary structure of a ribonuclease from bovine brain.
A;Reference number: JX0056; MUID:89214015; PMID:3243767
A;Accession: JX0056
A;Molecule type: protein
A;Residues: 27-154,'S',156-166 <WAT>
A;Experimental source: brain
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase
F;38,67,145/Active site: His, Lys, His #status predicted
F;52-110,66-121,84-136,91-98/Disulfide bonds: #status predicted
F;88/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;155/Binding site: carbohydrate (Thr) (covalent) #status experimental
F;159/Binding site: carbohydrate (Ser) (covalent) #status experimental

  Query Match             22.0%;  Score 133.5;  DB 2;  Length 167;
  Best Local Similarity   31.4%;  Pred. No. 3.7e-06;
  Matches   38;  Conservative   17;  Mismatches   43;  Indels   23;  Gaps    7;

Qy           5 ATFQQKHI------INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINM 58
               | |:::|:       : |  || :|     :  |:|| ||||:  |   |||:|:
Db          32 AKFRRQHMDSGSSSSSNPNYCNQMMKRR-RMTHGRCKPVNTFVHESLDDVKAVCS---QK 87

Qy          59 NVL----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHFA 105
               |:          | :  :  |  |  :  | | | :  :  || | || | | ||||
Db          88 NITCKNGHPNCYQSKSTMSITDCRETGSSKYPNCAYKTSQKQKYITVACEGNPYVPVHFD 147

Qy         106 G 106
               |
Db         148 G 148


RESULT 8
NRPG
pancreatic ribonuclease (EC 3.1.27.5) - pig
N;Alternate names: RNase 1; RNase A
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
C;Accession: A92071; A91391; A00816
R;Jackson, R.L.; Hirs, C.H.W.
J. Biol. Chem. 245, 637-653, 1970
A;Title: The primary structure of porcine pancreatic ribonuclease. II. The amino acid se
A;Reference number: A92071; MUID:70104197; PMID:5460946
A;Accession: A92071
A;Molecule type: protein
A;Residues: 1,'Q',3-124 <JAC>
R;Wierenga, R.K.; Huizinga, J.D.; Gaastra, W.; Welling, G.W.; Beintema, J.J.
FEBS Lett. 31, 181-185, 1973
A;Title: Affinity chromatography of porcine pancreatic ribonuclease and reinvestigation
A;Reference number: A91391
A;Accession: A91391
A;Molecule type: protein
A;Residues: 1-124 <WIE>
R;Phelan, J.J.; Hirs, C.H.W.
J. Biol. Chem. 245, 654-661, 1970
A;Title: The primary structure of porcine pancreatic ribonuclease. III. The disulfide bo
A;Reference number: A92072; MUID:70104198; PMID:4904878
A;Contents: annotation; disulfide bonds
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;21,34,76/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status experimental

  Query Match             21.9%;  Score 132.5;  DB 1;  Length 124;
  Best Local Similarity   31.6%;  Pred. No. 3.4e-06;
  Matches   36;  Conservative   19;  Mismatches   42;  Indels   17;  Gaps    6;

Qy           7 FQQKHI------INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGV-INMN 59
               ||::|:       |:   || :|     :  |:|| ||||:  |   |:|:|: : :|
Db           8 FQRQHMDPDSSSSNSSNYCNLMMSRR-NMTQGRCKPVNTFVHESLADVQAVCSQINVNCK 66

Qy          60 VLSTTRFQLNT------CTRTSITPRP-CPYSSRTETNYICVKCENQ--YPVHF 104
                 |  :| |:       | :|  :  | | | :  |  :| | ||     ||||
Db          67 NGQTNCYQSNSTMHITDCRQTGSSKYPNCAYKASQEQKHIIVACEGNPPVPVHF 120


RESULT 9
S41111
pancreatic ribonuclease - common iguana
C;Species: Iguana iguana (common iguana)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Aug-1998
C;Accession: S41111
R;Zhao, W.; Beintema, J.J.; Hofsteenge, J.
Eur. J. Biochem. 219, 641-646, 1994
A;Title: The amino acid sequence of iguana (Iguana iguana) pancreatic ribonuclease.
A;Reference number: S41111; MUID:94139745; PMID:8307028
A;Accession: S41111
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-119 <ZHA>
C;Superfamily: pancreatic ribonuclease

  Query Match             20.9%;  Score 126.5;  DB 2;  Length 119;
  Best Local Similarity   29.8%;  Pred. No. 1.3e-05;
  Matches   34;  Conservative   16;  Mismatches   51;  Indels   13;  Gaps    4;

Qy           3 NWATFQQKHI-------INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAIC--- 52
               :|::|| |||        |    |: :|     :   :|| |||: :| : :: :|
Db           2 DWSSFQNKHIDYPETSASNPNAYCDLMMQRR-NLNPTKCKTRNTFVHASPSEIQQVCGSG 60

Qy          53 -TGVINMNVLSTTRFQLNTCTRTSIT-PRPCPYSSRTETNYICVKCENQYPVHF 104
                |   :    |   | |  |      | |  | |:    |  | : |||  ||||
Db          61 GTHYEDNLYDSNESFDLTDCKNVGGTAPSSCKYNGTPGTKRIRIACENNQPVHF 114


RESULT 10
NRPRH
pancreatic ribonuclease (EC 3.1.27.5) - pronghorn (tentative sequence)
N;Alternate names: RNase 1; RNase A
C;Species: Antilocapra americana (pronghorn)
C;Date: 28-Feb-1981 #sequence_revision 28-Feb-1981 #text_change 31-Mar-2000
C;Accession: A00813
R;Beintema, J.J.; Gaastra, W.; Munniksma, J.
J. Mol. Evol. 13, 305-316, 1979
A;Title: Primary structure of pronghorn pancreatic ribonuclease: close relationship betw
A;Reference number: A00813; MUID:80075014; PMID:513141
A;Accession: A00813
A;Molecule type: protein
A;Residues: 1-124 <BEI>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F;34/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

  Query Match             20.2%;  Score 122.5;  DB 1;  Length 124;
  Best Local Similarity   30.3%;  Pred. No. 3.4e-05;
  Matches   36;  Conservative   18;  Mismatches   42;  Indels   23;  Gaps    7;

Qy           5 ATFQQKHIINTPI------ICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINM 58
               | |:::|| : |        || :| :   :  |:|| ||||:  |   |:|:|:
```

```
Qy          3 NWATFQQKHIINTP-IICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGV-INMNV 60
              ||| ||:||| ||  | |||||| :||||||||  ||||||||||||||:|   | ||
Db          2 NWAKFQEKHIPNTSNINCNTIMDKSIYIVGGQCKERNTFIISSATTVKAICSGASTNRNV 61

Qy         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              |||||||||| |::  |||||:|||||| |||||||: ||||||||||
Db         62 LSTTRFQLNTCIRSATAPRPCPYNSRTETNVICVKCENRLPVHFAGIGRC 111


RESULT 3
JX0085
pancreatic ribonuclease (EC 3.1.27.5) - bullfrog
C;Species: Rana catesbeiana (bullfrog)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994
C;Accession: JX0085
R;Nitta, R.; Katayama, N.; Okabe, Y.; Iwama, M.; Watanabe, H.; Abe, Y.; Okazaki, T.; Ohg
J. Biochem. 106, 729-735, 1989
A;Title: Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver.
A;Reference number: JX0085; MUID:90130374; PMID:2613682
A;Accession: JX0085
A;Molecule type: protein
A;Residues: 1-111 <NIT>
C;Superfamily: pancreatic ribonuclease
C;Keywords: hydrolase; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10,35,104/Active site: His, Lys, His #status predicted
F;19-72,34-82,52-97,94-111/Disulfide bonds: #status predicted

  Query Match             60.9%;  Score 369;  DB 2;  Length 111;
  Best Local Similarity   65.5%;  Pred. No. 1e-29;
  Matches   72;  Conservative    9;  Mismatches   27;  Indels    2;  Gaps    2;

Qy          3 NWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMNV 60
              ||| |::||| :|  | ||||||  ||||||:||  |||||||   |||||:||  :
Db          2 NWAKFKEKHIRSTSSIDCNTIMDKAIYIVGGKCKERNTFIISSEDNVKAICSGVSPDRKE 61

Qy         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              |||| |:|||| | |||||||||    : | |||||| | |||| |||:|
Db         62 LSTTSFKLNTCIRDSITPRPCPYHPSPDNNKICVKCEKQLPVHFVGIGKC 111


RESULT 4
A39035
ribonuclease-related anti-tumor protein - northern leopard frog (fragment)
C;Species: Rana pipiens (northern leopard frog)
C;Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993
C;Accession: A39035
R;Ardelt, W.; Mikulski, S.M.; Shogen, K.
J. Biol. Chem. 266, 245-251, 1991
A;Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and earl
A;Reference number: A39035; MUID:91093131; PMID:1985896
A;Accession: A39035
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-104 <ARD>
C;Superfamily: pancreatic ribonuclease

  Query Match             45.0%;  Score 272.5;  DB 2;  Length 104;
  Best Local Similarity   49.1%;  Pred. No. 3.6e-20;
  Matches   54;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          3 NWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMNV 60
              :| |||:||| ||  : |: ||  |::     ||  |||| |    ||||| |:| : ||
Db          2 DWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV 57

Qy         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              |:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         58 LTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104


RESULT 5
NRWHK
pancreatic ribonuclease (EC 3.1.27.5) - minke whale
N;Alternate names: RNase 1; RNase A
C;Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
C;Accession: A00818
R;Emmens, M.; Welling, G.W.; Beintema, J.J.
Biochem. J. 157, 317-323, 1976
A;Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclease.
A;Reference number: A00818; MUID:76277855; PMID:962870
A;Accession: A00818
A;Molecule type: protein
A;Residues: 1-124 <EMM>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F;76/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

  Query Match             22.4%;  Score 135.5;  DB 1;  Length 124;
  Best Local Similarity   33.3%;  Pred. No. 1.7e-06;
  Matches   39;  Conservative   16;  Mismatches   39;  Indels   23;  Gaps    7;

Qy          7 FQQKHII------NTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60
              ||:|:|:       | |  || :|     :  |:|| ||||:  |   |||:|:     ||
Db          8 FQRQHMDSGNSPGNNPNYCNQMMMRR-KMTQGRCKPVNTFVHESLEDVKAVCS---QKNV 63

Qy         61 L----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 104
              |          | :   :  | :|  :  | | | :  :  :| | || | | ||||
Db         64 LCKNGRTNCYESNSTMHITDCRQTGSSKYPNCAYKTSQKEKHIIVACEGNPYVPVHF 120


RESULT 6
A35932
angiogenin precursor - mouse
N;Alternate names: angiogenesis factor
N;Contains: ribonuclease (EC 3.1.27.-)
C;Species: Mus musculus (house mouse)
C;Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 18-Jun-1999
C;Accession: A35932
R;Bond, M.D.; Vallee, B.L.
Biochem. Biophys. Res. Commun. 171, 988-995, 1990
A;Title: Isolation and sequencing of mouse angiogenin DNA.
A;Reference number: A35932; MUID:91025023; PMID:2222458
A;Accession: A35932
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-145 <BON>
A;Cross-references: GB:U22516; NID:g726325; PIDN:AAA91366.1; PID:g726326
C;Genetics:
A;Introns: #status absent
C;Function:
A;Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues
C;Superfamily: pancreatic ribonuclease
C;Keywords: angiogenesis; hydrolase; nucleic acid degradation; pyroglutamic acid
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-145/Product: angiogenin #status predicted <MAT>
F;25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;37,64,137/Active site: His, Lys, His #status predicted
F;50-104,63-115,81-130/Disulfide bonds: #status predicted

  Query Match             22.4%;  Score 135.5;  DB 1;  Length 145;
  Best Local Similarity   39.5%;  Pred. No. 2e-06;
  Matches   30;  Conservative   12;  Mismatches   29;  Indels    5;  Gaps    3;

Qy         34 CKRVNTFIISSATTVKAIC---TGVINMNV-LSTTRFQLNTCTRTSITPR-PCPYSSRTE 88
              || |||||  : : :|||||         |: :| : ||: ||  |  :|| || | :
Db         63 CKDVNTFIHGNKSNIKAICGANGSPYRENLRMSKSPFQVTTCKHTGGSPRPPCQYRASAG 122

Qy         89 TNYICVKCENQYPVHF 104
                :: : |||  ||||
Db        123 FRHVVIACENGLPVHF 138


RESULT 7
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 11, 2004, 14:31:13 ; Search time 13.5611 Seconds
(without alignments)
787.345 Million cell updates/sec

Title: US-09-961-400-26
Perfect score: 606
Sequence: 1 MSNWATFQQKHIINTPIICN.....ICVKCENQYPVHFAGIGRCP 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	586.5	96.8	111	2	A27121	ribonuclease-relat
2	450	74.3	111	1	JX0120	ribonuclease-relat
3	369	60.9	111	2	JX0085	pancreatic ribonuc
4	272.5	45.0	104	2	A39035	ribonuclease-relat
5	135.5	22.4	124	1	NRWHK	pancreatic ribonuc
6	135.5	22.4	145	1	A35932	angiogenin precurs
7	133.5	22.0	167	2	S20066	pancreatic-type ri
8	132.5	21.9	124	1	NRPG	pancreatic ribonuc
9	126.5	20.9	119	2	S41111	pancreatic ribonuc
10	122.5	20.2	124	1	NRPRH	pancreatic ribonuc
11	122	20.1	122	1	NRKGR	pancreatic ribonuc
12	120.5	19.9	128	1	NRCU	pancreatic ribonuc
13	120.5	19.9	149	1	NRMS	pancreatic ribonuc
14	119.5	19.7	123	1	A43825	angiogenin - pig
15	118.5	19.6	128	1	NRGPB	pancreatic ribonuc
16	117.5	19.4	128	1	NRHO	pancreatic ribonuc
17	116.5	19.2	124	1	NRCM	pancreatic ribonuc
18	116.5	19.2	124	1	NRCMM	pancreatic ribonuc
19	116.5	19.2	124	1	NRCMB	pancreatic ribonuc
20	116.5	19.2	128	1	NRKS	pancreatic ribonuc
21	114.5	18.9	124	2	S08549	ribonuclease - dom
22	114	18.8	125	1	A32474	angiogenin [valida
23	113.5	18.7	124	1	NRDEN	pancreatic ribonuc
24	113.5	18.7	125	1	B43825	angiogenin - rabbi
25	113	18.6	147	1	NRHUAG	angiogenin precurs
26	112.5	18.6	124	1	NRGF	pancreatic ribonuc
27	112.5	18.6	124	1	NRDEO	pancreatic ribonuc
28	111.5	18.4	130	2	S22808	pancreatic ribonuc
29	110.5	18.2	124	1	NRBOB	pancreatic ribonuc
30	110.5	18.2	124	1	NRWB	pancreatic ribonuc
31	110.5	18.2	124	1	NREKN	pancreatic ribonuc
32	110.5	18.2	124	2	S07141	pancreatic ribonuc
33	110.5	18.2	150	1	NRBO	pancreatic ribonuc
34	110.5	18.2	158	2	I61900	eosinophil-derived
35	109.5	18.1	124	1	NRSH	pancreatic ribonuc
36	108.5	17.9	119	2	JX0115	pancreatic ribonuc
37	108.5	17.9	124	1	NRCB	pancreatic ribonuc
38	108.5	17.9	152	1	NRRT	pancreatic ribonuc
39	106.5	17.6	124	1	NRHP	pancreatic ribonuc
40	106.5	17.6	125	4	A47498	seminal ribonuclea
41	106.5	17.6	150	1	NRBOS	seminal ribonuclea
42	104.5	17.2	124	1	NRGN	pancreatic ribonuc
43	104.5	17.2	124	1	NRDEF	pancreatic ribonuc
44	104	17.2	125	2	S04503	pancreatic ribonuc
45	103.5	17.1	124	2	S08546	pancreatic ribonuc

ALIGNMENTS

RESULT 1
A27121
ribonuclease-related sialic acid-binding lectin - bullfrog
C;Species: Rana catesbeiana (bullfrog)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 30-Jun-1993
C;Accession: A27121
R;Titani, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kawauchi, H.; Takayanagi
Biochemistry 26, 2189-2194, 1987
A;Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana)
A;Reference number: A27121; MUID:87299649; PMID:3304421
A;Accession: A27121
A;Molecule type: protein
A;Residues: 1-111 <TIT>
C;Superfamily: pancreatic ribonuclease
C;Keywords: lectin

Query Match 96.8%; Score 586.5; DB 2; Length 111;
Best Local Similarity 99.1%; Pred. No. 2.5e-51;
Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```
Qy          3 NWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 61
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db          2 NWATFQQKHIINTPIINCNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 61

Qy         62 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
```

RESULT 2
JX0120
ribonuclease-related sialic acid-binding lectin - Japanese frog
C;Species: Rana japonica (Japanese frog)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JX0120
R;Kamiya, Y.; Oyama, F.; Oyama, R.; Sakakibara, F.; Nitta, K.; Kawauchi, H.; Takayanagi,
J. Biochem. 108, 139-143, 1990
A;Title: Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs.
A;Reference number: JX0120; MUID:91035319; PMID:2229005
A;Accession: JX0120
A;Molecule type: protein
A;Residues: 1-111 <KAM>
A;Experimental source: egg
C;Superfamily: pancreatic ribonuclease
C;Keywords: lectin; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;19-72,34-82,52-97,94-111/Disulfide bonds: #status experimental

Query Match 74.3%; Score 450; DB 1; Length 111;
Best Local Similarity 78.2%; Pred. No. 9e-38;
Matches 86; Conservative 7; Mismatches 15; Indels 2; Gaps 2;

PT Ribonuclease molecules based on native Onconase - used for killing cells,
PT particularly tumour cells.
XX
PS Disclosure; Page 75; 90pp; English.
XX
CC Sequences AAW35125 to AAW35135 represent recombinant fusion proteins
CC (rOnc) which are modifications of the RNase Onconase (RTM) (nOnc). Such
CC novel ribonuclease molecules are highly cytotoxic and can be used alone
CC or to form chemical conjugates or to target recombinant immunofusions.
CC They are used particularly for decreasing tumour cell growth. They can
CC also be used for cell separation in vitro by selectively killing unwanted
CC types of cells, e.g. in bone marrow prior to transplantation into a
CC patient undergoing marrow ablation by radiation, or for killing leukaemia
CC cells or T-cells that would cause graft versus host disease. The toxins
CC can also be used to selectively kill unwanted cells in culture. The new
CC ribonucleases have increased cytotoxic activity compared to nOnc and also
CC lower immunogenicity in humans
XX
SQ Sequence 355 AA;

Query Match 46.5%; Score 281.5; DB 2; Length 355;
Best Local Similarity 50.0%; Pred. No. 1.3e-23;
Matches 56; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

```
Qy          1 MSNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NM 58
              ||:| |||:||| ||  : |: ||  |::     ||  |||| |    ||||| |:| :
Db          1 MSDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASK 56

Qy         59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              |||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         57 NVLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 105
```

RESULT 15
AAW35129
ID AAW35129 standard; protein; 355 AA.
XX
AC AAW35129;
XX
DT 20-APR-1998 (first entry)
XX
DE R. pipiens recombinant RNase rOnc fusion protein 5.
XX
KW RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion;
KW tumour cell growth; frog.
XX
OS Rana pipiens.
OS Synthetic.
XX
PN WO9731116-A2.
XX
PD 28-AUG-1997.
XX
PF 19-FEB-1997; 97WO-US002588.
XX
PR 21-FEB-1996; 96US-0011800P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rybak SM, Newton DL, Boque L, Wlodawer A;
XX
DR WPI; 1997-435168/40.
DR N-PSDB; AAT94967.
XX
PT Ribonuclease molecules based on native Onconase - used for killing cells,
PT particularly tumour cells.
XX
PS Disclosure; Page 71; 90pp; English.
XX
CC Sequences AAW35125 to AAW35135 represent recombinant fusion proteins
CC (rOnc) which are modifications of the RNase Onconase (RTM) (nOnc). Such
CC novel ribonuclease molecules are highly cytotoxic and can be used alone
CC or to form chemical conjugates or to target recombinant immunofusions.
CC They are used particularly for decreasing tumour cell growth. They can
CC also be used for cell separation in vitro by selectively killing unwanted
CC types of cells, e.g. in bone marrow prior to transplantation into a
CC patient undergoing marrow ablation by radiation, or for killing leukaemia
CC cells or T-cells that would cause graft versus host disease. The toxins
CC can also be used to selectively kill unwanted cells in culture. The new
CC ribonucleases have increased cytotoxic activity compared to nOnc and also
CC lower immunogenicity in humans
XX
SQ Sequence 355 AA;

Query Match 46.5%; Score 281.5; DB 2; Length 355;
Best Local Similarity 50.0%; Pred. No. 1.3e-23;
Matches 56; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

```
Qy          1 MSNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NM 58
              ||:| |||:||| ||  : |: ||  |::     ||  |||| |    ||||| |:| :
Db        251 MSDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASK 306

Qy         59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              |||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db        307 NVLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 355
```

Search completed: May 11, 2004, 14:34:32
Job time : 50.7285 secs

```
OS   Rana pipiens.
OS   Synthetic.
XX
PN   WO9731116-A2.
XX
PD   28-AUG-1997.
XX
PF   19-FEB-1997;   97WO-US002588.
XX
PR   21-FEB-1996;   96US-0011800P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL,  Boque L,  Wlodawer A;
XX
DR   WPI; 1997-435168/40.
DR   N-PSDB; AAT94972.
XX
PT   Ribonuclease molecules based on native Onconase - used for killing cells,
PT   particularly tumour cells.
XX
PS   Disclosure; Page 76; 90pp; English.
XX
CC   Sequences AAW35125 to AAW35135 represent recombinant fusion proteins
CC   (rOnc) which are modifications of the RNase Onconase (RTM) (nOnc). Such
CC   novel ribonuclease molecules are highly cytotoxic and can be used alone
CC   or to form chemical conjugates or to target recombinant immunofusions.
CC   They are used particularly for decreasing tumour cell growth. They can
CC   also be used for cell separation in vitro by selectively killing unwanted
CC   types of cells, e.g. in bone marrow prior to transplantation into a
CC   patient undergoing marrow ablation by radiation, or for killing leukaemia
CC   cells or T-cells that would cause graft versus host disease. The toxins
CC   can also be used to selectively kill unwanted cells in culture. The new
CC   ribonucleases have increased cytotoxic activity compared to nOnc and also
CC   lower immunogenicity in humans
XX
SQ   Sequence 251 AA;

  Query Match             46.5%;  Score 281.5;  DB 2;  Length 251;
  Best Local Similarity   50.0%;  Pred. No. 8.7e-24;
  Matches   56;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          1 MSNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NM 58
              ||:| |||:||| ||  : |: ||  |::     ||  |||| |    ||||| |:| :
Db        147 MSDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASK 202

Qy         59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              |||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db        203 NVLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 251


RESULT 13
AAW35135
ID   AAW35135 standard; protein; 254 AA.
XX
AC   AAW35135;
XX
DT   20-APR-1998  (first entry)
XX
DE   R. pipiens recombinant RNase rOnc fusion protein 11.
XX
KW   RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion;
KW   tumour cell growth; frog.
XX
OS   Rana pipiens.
OS   Synthetic.
XX
PN   WO9731116-A2.
XX
PD   28-AUG-1997.
XX
PF   19-FEB-1997;   97WO-US002588.
XX
PR   21-FEB-1996;   96US-0011800P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL,  Boque L,  Wlodawer A;
XX
DR   WPI; 1997-435168/40.
DR   N-PSDB; AAT94973.
XX
PT   Ribonuclease molecules based on native Onconase - used for killing cells,
PT   particularly tumour cells.
XX
PS   Disclosure; Page 77; 90pp; English.
XX
CC   Sequences AAW35125 to AAW35135 represent recombinant fusion proteins
CC   (rOnc) which are modifications of the RNase Onconase (RTM) (nOnc). Such
CC   novel ribonuclease molecules are highly cytotoxic and can be used alone
CC   or to form chemical conjugates or to target recombinant immunofusions.
CC   They are used particularly for decreasing tumour cell growth. They can
CC   also be used for cell separation in vitro by selectively killing unwanted
CC   types of cells, e.g. in bone marrow prior to transplantation into a
CC   patient undergoing marrow ablation by radiation, or for killing leukaemia
CC   cells or T-cells that would cause graft versus host disease. The toxins
CC   can also be used to selectively kill unwanted cells in culture. The new
CC   ribonucleases have increased cytotoxic activity compared to nOnc and also
CC   lower immunogenicity in humans
XX
SQ   Sequence 254 AA;

  Query Match             46.5%;  Score 281.5;  DB 2;  Length 254;
  Best Local Similarity   50.0%;  Pred. No. 8.8e-24;
  Matches   56;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          1 MSNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NM 58
              ||:| |||:||| ||  : |: ||  |::     ||  |||| |    ||||| |:| :
Db          1 MSDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASK 56

Qy         59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              |||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         57 NVLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 105


RESULT 14
AAW35133
ID   AAW35133 standard; protein; 355 AA.
XX
AC   AAW35133;
XX
DT   20-APR-1998  (first entry)
XX
DE   R. pipiens recombinant RNase rOnc fusion protein 9.
XX
KW   RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion;
KW   tumour cell growth; frog.
XX
OS   Rana pipiens.
OS   Synthetic.
XX
PN   WO9731116-A2.
XX
PD   28-AUG-1997.
XX
PF   19-FEB-1997;   97WO-US002588.
XX
PR   21-FEB-1996;   96US-0011800P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL,  Boque L,  Wlodawer A;
XX
DR   WPI; 1997-435168/40.
DR   N-PSDB; AAT94971.
XX
```

```
RESULT 10
AAY28867
ID   AAY28867 standard; protein; 105 AA.
XX
AC   AAY28867;
XX
DT   25-JAN-2000  (first entry)
XX
DE   Recombinant Met(-1) RaPLR1.
XX
KW   Recombinant Met(-1) Rana pipiens ribonuclease; RaPLR1; CD22; RNase;
KW   covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
KW   Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
KW   recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
KW   autoimmune disease.
XX
OS   Rana pipiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
FT                   /note= "Met not found in wild type RaPLR1"
XX
PN   WO9950398-A2.
XX
PD   07-OCT-1999.
XX
PF   26-MAR-1999;   99WO-US006641.
XX
PR   27-MAR-1998;   98US-0079751P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL;
XX
DR   WPI; 1999-610847/52.
DR   N-PSDB; AAZ08126.
XX
PT   New recombinant ribonucleases, used for killing target cells, e.g. for
PT   treating cancers, viral infections or autoimmune diseases.
XX
PS   Claim 34; Page 57; 71pp; English.
XX
CC   The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1)
CC   protein with Met at position 1. Carboxy terminal end of recombinant
CC   RaPLR1 has a covalently bound ligand binding moiety, which can be a LL2
CC   antibody directed against CD22 on cancerous B cells or human chorionic
CC   gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant
CC   ribonucleases can be expressed in bacteria without an N-terminal
CC   methionine due to the presence of a signal peptide that is cleaved by
CC   bacteria. The soluble expression of ribonuclease allows the proteins to
CC   be fused in-frame with ligand binding moieties to form cytotoxic fusion
CC   proteins. They can be used for treatment of cancer and autoimmune
CC   diseases
XX
SQ   Sequence 105 AA;

  Query Match             46.5%;  Score 281.5;  DB 2;  Length 105;
  Best Local Similarity   49.1%;  Pred. No. 2.9e-24;
  Matches   55;  Conservative   15;  Mismatches   33;  Indels    9;  Gaps    4;

Qy          1 MSNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NM 58
              | :| |||:||: ||  : || ||  |::     ||  |||| |    ||||| |:| :
Db          1 MQDWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASK 56

Qy         59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              |||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         57 NVLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105


RESULT 11
AAW35118
ID   AAW35118 standard; protein; 112 AA.
XX
AC   AAW35118;
XX
DT   20-APR-1998  (first entry)
XX
DE   R. pipiens recombinant RNase protein NLSMetSerrOnc.
XX
KW   RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion;
KW   tumour cell growth; frog.
XX
OS   Rana pipiens.
XX
PN   WO9731116-A2.
XX
PD   28-AUG-1997.
XX
PF   19-FEB-1997;   97WO-US002588.
XX
PR   21-FEB-1996;   96US-0011800P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL,  Boque L,  Wlodawer A;
XX
DR   WPI; 1997-435168/40.
DR   N-PSDB; AAT94955.
XX
PT   Ribonuclease molecules based on native Onconase - used for killing cells,
PT   particularly tumour cells.
XX
PS   Claim 18; Page 63; 90pp; English.
XX
CC   AAW35115 to AAW35123 encode recombinant proteins (rOnc) which are
CC   modifications of the RNase Onconase (RTM) (nOnc). Such novel ribonuclease
CC   molecules are highly cytotoxic and can be used alone or to form chemical
CC   conjugates or to target recombinant immunofusions. They are used
CC   particularly for decreasing tumour cell growth. They can also be used for
CC   cell separation in vitro by selectively killing unwanted types of cells,
CC   e.g. in bone marrow prior to transplantation into a patient undergoing
CC   marrow ablation by radiation, or for killing leukaemia cells or T-cells
CC   that would cause graft versus host disease. The toxins can also be used
CC   to selectively kill unwanted cells in culture. The new ribonucleases have
CC   increased cytotoxic activity compared to nOnc and also lower
CC   immunogenicity in humans
XX
SQ   Sequence 112 AA;

  Query Match             46.5%;  Score 281.5;  DB 2;  Length 112;
  Best Local Similarity   50.0%;  Pred. No. 3.2e-24;
  Matches   56;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          1 MSNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NM 58
              ||:| |||:||| ||  : |: ||  |::     ||  |||| |    ||||| |:| :
Db          8 MSDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASK 63

Qy         59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              |||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         64 NVLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 112


RESULT 12
AAW35134
ID   AAW35134 standard; protein; 251 AA.
XX
AC   AAW35134;
XX
DT   20-APR-1998  (first entry)
XX
DE   R. pipiens recombinant RNase rOnc fusion protein 10.
XX
KW   RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion;
KW   tumour cell growth; frog.
XX
```

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CC   (Rana catesbeiana) lectin used to describe the method of the invention
XX
SQ   Sequence 111 AA;

  Query Match             96.8%;  Score 586.5;  DB 2;  Length 111;
  Best Local Similarity   99.1%;  Pred. No. 3.6e-59;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          3 NWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 61
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db          2 NWATFQQKHIINTPIINCNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 61

Qy         62 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111


RESULT 8
AAY28871
ID   AAY28871 standard; protein; 105 AA.
XX
AC   AAY28871;
XX
DT   25-JAN-2000  (first entry)
XX
DE   Recombinant Met(-1) RaPLR1 Gln1Ser amino acid sequence.
XX
KW   Recombinant Met(-1) Rana pipiens ribonuclease Gln1Ser; RaPLR1; CD22;
KW   covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
KW   Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
KW   recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
KW   autoimmune disease; RNase.
XX
OS   Rana pipiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
FT                   /note= "Met not found in wild type RaPLR1"
FT   Misc-difference 2
FT                   /note= "Wild type Gln replaced with Ser"
XX
PN   WO9950398-A2.
XX
PD   07-OCT-1999.
XX
PF   26-MAR-1999;   99WO-US006641.
XX
PR   27-MAR-1998;   98US-0079751P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL;
XX
DR   WPI; 1999-610847/52.
DR   N-PSDB; AAZ08129.
XX
PT   New recombinant ribonucleases, used for killing target cells, e.g. for
PT   treating cancers, viral infections or autoimmune diseases.
XX
PS   Claim 34; Page 61; 71pp; English.
XX
CC   The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1)
CC   protein with Met at position 1 and Gln2Ser. Carboxy terminal end of
CC   recombinant RaPLR1 has a covalently bound ligand binding moiety, which
CC   can be a LL2 antibody directed against CD22 on cancerous B cells or human
CC   chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells.
CC   Recombinant ribonucleases can be expressed in bacteria without an N-
CC   terminal methionine due to the presence of a signal peptide that is
CC   cleaved by bacteria. The soluble expression of ribonuclease allows the
CC   proteins to be fused in-frame with ligand binding moieties to form
CC   cytotoxic fusion proteins. They can be used for treatment of cancer and
CC   autoimmune diseases
XX
SQ   Sequence 105 AA;

  Query Match             47.1%;  Score 285.5;  DB 2;  Length 105;
  Best Local Similarity   50.0%;  Pred. No. 1e-24;
  Matches   56;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          1 MSNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NM 58
              ||:| |||:||: ||  : || ||  |::     ||  |||| |    |||| |:| :
Db          1 MSDWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASK 56

Qy         59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              |||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         57 NVLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105


RESULT 9
AAW06544
ID   AAW06544 standard; protein; 104 AA.
XX
AC   AAW06544;
XX
DT   22-AUG-1997  (first entry)
XX
DE   Antitumour protein from Rana pipiens oocytes.
XX
KW   Tumour; chemotherapy; radiotherapy; frog.
XX
OS   Rana pipiens.
XX
PN   WO9639428-A1.
XX
PD   12-DEC-1996.
XX
PF   03-JUN-1996;   96WO-US008304.
XX
PR   06-JUN-1995;   95US-00467955.
XX
PA   (ALFA-) ALFACELL CORP.
XX
PI   Ardelt WJ;
XX
DR   WPI; 1997-043063/04.
XX
PT   Antitumour proteins from Rana pipiens oocyte(s) - have fewer
PT   disadvantages than chemotherapy, surgery and radiotherapy.
XX
PS   Claim 8; Page 28; 45pp; English.
XX
CC   The present sequence is a specifically claimed example of an antitumour
CC   protein from the generic protein in AAW18224, with the molecular weight
CC   12000. This is one of two preferred proteins (the other in AAW06543) that
CC   have been isolated from Rana pipiens oocytes. Both proteins have a
CC   blocked amino terminal group and are essentially free of carbohydrates.
CC   The proteins are used to treat tumours. Use of the peptides has fewer
CC   disadvantages than chemotherapy, radiotherapy and surgery in the
CC   treatment of tumours
XX
SQ   Sequence 104 AA;

  Query Match             46.6%;  Score 282.5;  DB 2;  Length 104;
  Best Local Similarity   50.0%;  Pred. No. 2.2e-24;
  Matches   55;  Conservative   15;  Mismatches   31;  Indels    9;  Gaps    4;

Qy          3 NWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMNV 60
              :| |||:||: ||  : || ||  |::     ||  |||| |    ||||| |:| : ||
Db          2 DWLTFQKKHVTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV 57

Qy         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              |:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:|||
Db         58 LTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGRC 104
```

```
SQ   Sequence 111 AA;

  Query Match             98.3%;  Score 596;  DB 2;  Length 111;
  Best Local Similarity   97.3%;  Pred. No. 3e-60;
  Matches  108;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MSNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60
              | |||||||||||||||||||:|||||||||||||||||||||||||||||||:||
Db          1 MQNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 60

Qy         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111


RESULT 6
AAY28874
ID   AAY28874 standard; protein; 110 AA.
XX
AC   AAY28874;
XX
DT   25-JAN-2000  (first entry)
XX
DE   Recombinant RaCOR1 Met22Leu Met57Leu amino acid sequence.
XX
KW   Recombinant Rana catesbeiana oocyte ribonuclease; covalently bound;
KW   RaCOR1 Met22Leu Met57Leu; LL2 antibody; ligand binding moiety; CD22;
KW   cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG;
KW   signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
KW   cancer; bullfrog; RNase; autoimmune disease.
XX
OS   Rana catesbeiana.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 22
FT                   /note= "Wild type Met replaced with Leu"
FT   Misc-difference 57
FT                   /note= "Wild type Met replaced with Leu"
XX
PN   WO9950398-A2.
XX
PD   07-OCT-1999.
XX
PF   26-MAR-1999;   99WO-US006641.
XX
PR   27-MAR-1998;   98US-0079751P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL;
XX
DR   WPI; 1999-610847/52.
DR   N-PSDB; AAZ08132.
XX
PT   New recombinant ribonucleases, used for killing target cells, e.g. for
PT   treating cancers, viral infections or autoimmune diseases.
XX
PS   Claim 22; Page 64; 71pp; English.
XX
CC   The present sequence is a recombinant Rana catesbeiana oocyte
CC   ribonuclease (RaCOR1) protein with Met22Leu Met57Leu. Carboxy terminal
CC   end of recombinant RaCOR1 has a covalently bound ligand binding moiety,
CC   which can be a LL2 antibody directed against CD22 on cancerous B cells or
CC   human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma
CC   cells. Recombinant ribonucleases can be expressed in bacteria without an
CC   N-terminal methionine due to the presence of a signal peptide that is
CC   cleaved by bacteria. The soluble expression of ribonuclease allows the
CC   proteins to be fused in-frame with ligand binding moieties to form
CC   cytotoxic fusion proteins. They can be used for treatment of cancer and
CC   autoimmune diseases
XX
SQ   Sequence 110 AA;

  Query Match             97.5%;  Score 591;  DB 2;  Length 110;
  Best Local Similarity   98.2%;  Pred. No. 1.1e-59;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 NWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS 62
              |||||||||||||||||||:|||||||||||||||||||||||||||||||:||||
Db          2 NWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVLS 61

Qy         63 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110


RESULT 7
AAY33321
ID   AAY33321 standard; protein; 111 AA.
XX
AC   AAY33321;
XX
DT   29-NOV-1999  (first entry)
XX
DE   Frog lectin protein fragment.
XX
KW   Cytotoxic; RNase; ribonuclease; pancreatic; antibody; light chain;
KW   heavy chain; cell surface marker; treatment; tumor; viral infection;
KW   parasite infection; immune dysfunctional cell; autoimmune disease;
KW   contraceptive; cell separation; transplantation; bone marrow ablation;
KW   leukemia cell; T-cell; graft-versus-host disease; bullfrog; lectin.
XX
OS   Rana catesbeiana.
XX
PN   US5955073-A.
XX
PD   21-SEP-1999.
XX
PF   09-JUL-1997;   97US-00891848.
XX
PR   20-APR-1990;   90US-00510696.
PR   22-OCT-1991;   91US-00779195.
PR   04-FEB-1993;   93US-00014082.
PR   22-SEP-1993;   93US-00125462.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL,  Nicholls PJ,  Youle RJ;
XX
DR   WPI; 1999-560488/47.
XX
PT   Recombinantly fused pancreatic RNase-targeting proteins useful for
PT   treating tumors, infections, immune or autoimmune disorders and as a
PT   contraceptive.
XX
PS   Example 3; Fig 19; 47pp; English.
XX
CC   This invention describes a novel nucleic acid construct comprising
CC   sequences encoding functional pancreatic RNase and a second protein
CC   (preferably the light and heavy chains of an antibody) which binds a
CC   specific cell surface marker on a target cell and functions as a
CC   cytotoxic agent. The products can be used for selectively killing cells
CC   expressing a specific surface marker. They can be used for treating
CC   tumors or infected cells (e.g. cells infected by viruses (especially
CC   latent or chronic virus infections, such as human immunodeficiency virus
CC   (HIV)-1, Epstein-Barr virus, herpes viruses (herpes simplex types I and
CC   II), hepatitis viruses (B, non-A-non-B, and delta), herpes zoster,
CC   cytomegalovirus)) and cells infected with parasites (such as the malaria
CC   parasite)). They can also be used for treating immune dysfunctional cells
CC   in immune and autoimmune diseases. Additionally, they may be used as
CC   contraceptives. Finally they can also be used for cell separation in
CC   vitro by selectively killing unwanted types of cells (e.g. in bone
CC   marrow) prior to transplantation into a patient undergoing marrow
CC   ablation by radiation or for killing leukemia cells or T-cells that would
CC   cause graft-versus-host disease. This sequence represents a bullfrog
```

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CC   cytotoxic fusion proteins. They can be used for treatment of cancer and
CC   autoimmune diseases
XX
SQ   Sequence 110 AA;

  Query Match             99.2%;  Score 601;  DB 2;  Length 110;
  Best Local Similarity   100.0%;  Pred. No. 7.9e-61;
  Matches  110;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 SNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 60

Qy         62 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110


RESULT 4
AAY28872
ID   AAY28872 standard; protein; 110 AA.
XX
AC   AAY28872;
XX
DT   25-JAN-2000  (first entry)
XX
DE   Rana catesbeiana oocyte ribonuclease (RaCOR1) amino acid sequence.
XX
KW   Rana catesbeiana oocyte ribonuclease; RaCOR1; covalently bound; CD22;
KW   LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's Sarcoma;
KW   human chorionic gonadotrophin; hCG; recombinant ribonuclease; bullfrog;
KW   signal peptide; cytotoxic fusion protein; cancer; autoimmune disease;
KW   RNase.
XX
OS   Rana catesbeiana.
OS   Synthetic.
XX
PN   WO9950398-A2.
XX
PD   07-OCT-1999.
XX
PF   26-MAR-1999;   99WO-US006641.
XX
PR   27-MAR-1998;   98US-0079751P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL;
XX
DR   WPI; 1999-610847/52.
DR   N-PSDB; AAZ08130.
XX
PT   New recombinant ribonucleases, used for killing target cells, e.g. for
PT   treating cancers, viral infections or autoimmune diseases.
XX
PS   Claim 22; Page 62; 71pp; English.
XX
CC   The present sequence is a Rana catesbeiana oocyte ribonuclease (RaCOR1)
CC   protein encoded by a cDNA modified for expression in E. coli. Carboxy
CC   terminal end of RaCOR1 has a covalently bound ligand binding moiety,
CC   which can be a LL2 antibody directed against CD22 on cancerous B cells or
CC   human chorionic gonadotrophin (hCG) effective against Kaposi's Sarcoma
CC   cells. Recombinant ribonucleases can be expressed in bacteria without an
CC   N-terminal methionine due to the presence of a signal peptide that is
CC   cleaved by bacteria. The soluble expression of ribonuclease allows the
CC   proteins to be fused in-frame with ligand binding moieties to form
CC   cytotoxic fusion proteins. They can be used for treatment of cancer and
CC   autoimmune diseases
XX
SQ   Sequence 110 AA;

  Query Match             98.5%;  Score 597;  DB 2;  Length 110;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-60;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 NWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS 62
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 NWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS 61

Qy         63 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110


RESULT 5
AAY28876
ID   AAY28876 standard; protein; 111 AA.
XX
AC   AAY28876;
XX
DT   25-JAN-2000  (first entry)
XX
DE   Recombinant Met(-1) RaCOR1 Met22Leu Met57Leu-(His)6 protein.
XX
KW   Met(-1) Rana catesbeiana ribonuclease Met22Leu Met57Leu-(His)6; RaCOR1;
KW   recombinant; CD22; covalently bound; LL2 antibody; ligand binding moiety;
KW   cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG;
KW   signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
KW   cancer; bullfrog; RNase; autoimmune disease.
XX
OS   Rana catesbeiana.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
FT                   /note= "Met not found in wild type RaCOR1"
FT   Misc-difference 1
FT                   /note= "(His)6 histidine tag attached to N-terminal Met"
FT   Misc-difference 23
FT                   /note= "Wild type Met replaced with Leu"
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FT                   /note= "Wild type Met replaced with Leu"
XX
PN   WO9950398-A2.
XX
PD   07-OCT-1999.
XX
PF   26-MAR-1999;   99WO-US006641.
XX
PR   27-MAR-1998;   98US-0079751P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL;
XX
DR   WPI; 1999-610847/52.
DR   N-PSDB; AAZ08133.
XX
PT   New recombinant ribonucleases, used for killing target cells, e.g. for
PT   treating cancers, viral infections or autoimmune diseases.
XX
PS   Claim 22; Page 66; 71pp; English.
XX
CC   The present sequence is a recombinant Rana catesbeiana oocyte
CC   ribonuclease (RaCOR1) protein with Met at position 1 attached to a (His)6
CC   tag, Met23Leu and Met58Leu. Carboxy terminal end of recombinant RaCOR1
CC   has a covalently bound ligand binding moiety, which can be a LL2 antibody
CC   directed against CD22 on cancerous B cells or human chorionic
CC   gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant
CC   ribonucleases can be expressed in bacteria without an N-terminal
CC   methionine due to the presence of a signal peptide that is cleaved by
CC   bacteria. The soluble expression of ribonuclease allows the proteins to
CC   be fused in-frame with ligand binding moieties to form cytotoxic fusion
CC   proteins. They can be used for treatment of cancer and autoimmune
CC   diseases
XX
```

```
CC   can be a LL2 antibody directed against CD22 on cancerous B cells or human
CC   chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells.
CC   Recombinant ribonucleases can be expressed in bacteria without an N-
CC   terminal methionine due to the presence of a signal peptide that is
CC   cleaved by bacteria. The soluble expression of ribonuclease allows the
CC   proteins to be fused in-frame with ligand binding moieties to form
CC   cytotoxic fusion proteins. They can be used for treatment of cancer and
CC   autoimmune diseases
XX
SQ   Sequence 111 AA;

  Query Match             100.0%;  Score 606;  DB 2;  Length 111;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-61;
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Qy          1 MSNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60
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ID   AAY28873 standard; protein; 111 AA.
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AC   AAY28873;
XX
DT   25-JAN-2000  (first entry)
XX
DE   Recombinant Met(-1) RaCOR1.
XX
KW   Recombinant Met(-1) Rana catesbeiana oocyte ribonuclease; RaCOR1; CD22;
KW   covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
KW   Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
KW   recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;
KW   RNase; autoimmune disease.
XX
OS   Rana catesbeiana.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
FT                   /note= "Met not found in wild type RaCOR1"
XX
PN   WO9950398-A2.
XX
PD   07-OCT-1999.
XX
PF   26-MAR-1999;   99WO-US006641.
XX
PR   27-MAR-1998;   98US-0079751P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL;
XX
DR   WPI; 1999-610847/52.
DR   N-PSDB; AAZ08131.
XX
PT   New recombinant ribonucleases, used for killing target cells, e.g. for
PT   treating cancers, viral infections or autoimmune diseases.
XX
PS   Claim 22; Page 63; 71pp; English.
XX
CC   The present sequence is a recombinant Rana catesbeiana oocyte
CC   ribonuclease (RaCOR1) protein with Met at position 1. Carboxy terminal
CC   end of recombinant RaCOR1 has a covalently bound ligand binding moiety,
CC   which can be a LL2 antibody directed against CD22 on cancerous B cells or
CC   human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma
CC   cells. Recombinant ribonucleases can be expressed in bacteria without an
CC   N-terminal methionine due to the presence of a signal peptide that is
CC   cleaved by bacteria. The soluble expression of ribonuclease allows the
CC   proteins to be fused in-frame with ligand binding moieties to form
CC   cytotoxic fusion proteins. They can be used for treatment of cancer and
CC   autoimmune diseases
XX
SQ   Sequence 111 AA;

  Query Match             99.3%;  Score 602;  DB 2;  Length 111;
  Best Local Similarity   99.1%;  Pred. No. 6.1e-61;
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Qy          1 MSNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111


RESULT 3
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ID   AAY28877 standard; protein; 110 AA.
XX
AC   AAY28877;
XX
DT   25-JAN-2000  (first entry)
XX
DE   Recombinant RaCOR1 Gln1Ser amino acid sequence.
XX
KW   Recombinant Rana catesbeiana oocyte ribonuclease; RaCOR1 Gln1Ser; CD22;
KW   covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
KW   bullfrog; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; RNase;
KW   signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
KW   cancer; autoimmune disease.
XX
OS   Rana catesbeiana.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
FT                   /note= "Wild type Gln replaced with Ser"
XX
PN   WO9950398-A2.
XX
PD   07-OCT-1999.
XX
PF   26-MAR-1999;   99WO-US006641.
XX
PR   27-MAR-1998;   98US-0079751P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL;
XX
DR   WPI; 1999-610847/52.
DR   N-PSDB; AAZ08134.
XX
PT   New recombinant ribonucleases, used for killing target cells, e.g. for
PT   treating cancers, viral infections or autoimmune diseases.
XX
PS   Claim 22; Page 67; 71pp; English.
XX
CC   The present sequence is a recombinant Rana catesbeiana oocyte
CC   ribonuclease (RaCOR1) protein with Gln1Ser. Carboxy terminal end of
CC   recombinant RaCOR1 has a covalently bound ligand binding moiety, which
CC   can be a LL2 antibody directed against CD22 on cancerous B cells or human
CC   chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells.
CC   Recombinant ribonucleases can be expressed in bacteria without an N-
CC   terminal methionine due to the presence of a signal peptide that is
CC   cleaved by bacteria. The soluble expression of ribonuclease allows the
CC   proteins to be fused in-frame with ligand binding moieties to form
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 11, 2004, 14:23:43 ; Search time 50.7285 Seconds
(without alignments)
618.248 Million cell updates/sec

Title: US-09-961-400-26
Perfect score: 606
Sequence: 1 MSNWATFQQKHIINTPIICN.....ICVKCENQYPVHFAGIGRCP 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	602	99.3	111	2	AAY28873	Aay28873 Recombina
3	601	99.2	110	2	AAY28877	Aay28877 Recombina
4	597	98.5	110	2	AAY28872	Aay28872 Rana cate
5	596	98.3	111	2	AAY28876	Aay28876 Recombina
6	591	97.5	110	2	AAY28874	Aay28874 Recombina
7	586.5	96.8	111	2	AAY33321	Aay33321 Frog lect
8	285.5	47.1	105	2	AAY28871	Aay28871 Recombina
9	282.5	46.6	104	2	AAW06544	Aaw06544 Antitumou
10	281.5	46.5	105	2	AAY28867	Aay28867 Recombina
11	281.5	46.5	112	2	AAW35118	Aaw35118 R. pipien
12	281.5	46.5	251	2	AAW35134	Aaw35134 R. pipien
13	281.5	46.5	254	2	AAW35135	Aaw35135 R. pipien
14	281.5	46.5	355	2	AAW35133	Aaw35133 R. pipien
15	281.5	46.5	355	2	AAW35129	Aaw35129 R. pipien
16	281.5	46.5	366	2	AAW35132	Aaw35132 R. pipien
17	280.5	46.3	104	2	AAY28870	Aay28870 Recombina
18	278.5	46.0	105	2	AAY28869	Aay28869 Recombina
19	277.5	45.8	105	2	AAW35123	Aaw35123 R. pipien
20	277.5	45.8	105	2	AAY39400	Aay39400 Recombina
21	277.5	45.8	355	2	AAW35125	Aaw35125 R. pipien
22	277.5	45.8	358	2	AAW35130	Aaw35130 R. pipien
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24	276.5	45.6	105	2	AAW35116	Aaw35116 R. pipien
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26	273.5	45.1	104	2	AAY28866	Aay28866 Recombina
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28	272.5	45.0	104	2	AAR47303	Aar47303 ONCONASE
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31	272.5	45.0	104	2	AAW06543	Aaw06543 Antitumou
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33	272.5	45.0	104	2	AAW88233	Aaw88233 Rana pipi
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37	272.5	45.0	106	2	AAW35122	Aaw35122 R. pipien
38	272.5	45.0	107	2	AAW35117	Aaw35117 R. pipien
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ALIGNMENTS

RESULT 1
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ID AAY28878 standard; protein; 111 AA.
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AC AAY28878;
XX
DT 25-JAN-2000 (first entry)
XX
DE Recombinant Met(-1) RaCOR1 Gln1Ser amino acid sequence.
XX
KW Recombinant Met(-1) Rana catesbeiana oocyte ribonuclease Gln1Ser; RaCOR1;
KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
KW Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
KW recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;
KW CD22; RNase; autoimmune disease.
XX
OS Rana catesbeiana.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1
FT /note= "Met not found in wild type RaCOR1"
FT Misc-difference 2
FT /note= "Wild type Gln replaced with Ser"
XX
PN WO9950398-A2.
XX
PD 07-OCT-1999.
XX
PF 26-MAR-1999; 99WO-US006641.
XX
PR 27-MAR-1998; 98US-0079751P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rybak SM, Newton DL;
XX
DR WPI; 1999-610847/52.
DR N-PSDB; AAZ08135.
XX
PT New recombinant ribonucleases, used for killing target cells, e.g. for
PT treating cancers, viral infections or autoimmune diseases.
XX
PS Claim 22; Page 68; 71pp; English.
XX
CC The present sequence is a recombinant Rana catesbeiana ribonuclease
CC (RaCOR1) protein with Met at position 1 and Gln2Ser. Carboxy terminal end
CC of recombinant RaCOR1 has a covalently bound ligand binding moiety, which

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US-08-875-811-1
; Sequence 1, Application US/08875811
; Patent No. 6045793
;  GENERAL INFORMATION:
;    APPLICANT:  Rybak, Susanna M.
;    APPLICANT:  Newton, Dianne L.
;    APPLICANT:  Boque, Lluis
;    APPLICANT:  Wlodawer, Alexander
;    TITLE OF INVENTION:  Recombinant Ribonuclease Proteins
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/875,811
;      FILING DATE:  19-FEB-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/02588
;      FILING DATE:  19-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/011,800
;      FILING DATE:  21-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Faris, Susan K.
;      REGISTRATION NUMBER:  41,739
;      REFERENCE/DOCKET NUMBER:  015280-244100US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  104 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
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;      OTHER INFORMATION:  /note= "native ONCONASE (Registered
;      OTHER INFORMATION:  Trademark) from Rana pipiens"
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  1
;      OTHER INFORMATION:  /note= "Xaa = pyroglutamic acid"
US-08-875-811-1

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Qy         60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
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Search completed: May 11, 2004, 14:37:53
Job time : 16.4253 secs
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RESULT 13
US-08-467-955-1
; Sequence 1, Application US/08467955
; Patent No. 5728805
;  GENERAL INFORMATION:
;    APPLICANT:  Ardelt Ph.D, Wojciech J.
;    TITLE OF INVENTION:  PHARMACEUTICALS AND METHOD FOR MAKING THEM
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mark H. Jay, P.A.
;      STREET:  P.O. Box E
;      CITY:  Short Hills
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07078-0383
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/467,955
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/178,118
;      FILING DATE:  06-APR-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/436,141
;      FILING DATE:  13-NOV-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/814,332
;      FILING DATE:  03-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/283,970
;      FILING DATE:  01-AUG-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jay, Mark H.
;      REGISTRATION NUMBER:  27507
;      REFERENCE/DOCKET NUMBER:  5007 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-912-9066
;      TELEFAX:  201-912-0442
;      TELEX:  No. 5728805 Applicable
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  104 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  N
;    ANTI-SENSE:  N
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  Rana pipiens
;      DEVELOPMENTAL STAGE:  Oocyte
US-08-467-955-1

  Query Match             45.3%;  Score 272.5;  DB 1;  Length 104;
  Best Local Similarity   49.1%;  Pred. No. 3.5e-24;
  Matches   54;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          2 NWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMNV 59
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Db          2 DWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV 57

Qy         60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
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RESULT 14
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; Sequence 13, Application US/08891848
; Patent No. 5955073
;  GENERAL INFORMATION:
;    APPLICANT:  Rybak, Susanna M.
;    APPLICANT:  Youle, Richard J.
;    APPLICANT:  Newton, Dianne L.
;    APPLICANT:  Nicholls, Peter J.
;    TITLE OF INVENTION:  Selective RNase Cytotoxic Reagents
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/891,848
;      FILING DATE:  No. 5955073 yet assigned
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/125,462
;      FILING DATE:  22-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/014,082
;      FILING DATE:  04-FEB-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/779,195
;      FILING DATE:  22-OCT-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/510,696
;      FILING DATE:  20-APR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Weber, Ellen Lauver
;      REGISTRATION NUMBER:  32,762
;      REFERENCE/DOCKET NUMBER:  015280-110310US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  104 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  Protein
;      LOCATION:  1..104
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;      OTHER INFORMATION:  /note= "Onconase from Rana pipiens"
US-08-891-848-13

  Query Match             45.3%;  Score 272.5;  DB 2;  Length 104;
  Best Local Similarity   49.1%;  Pred. No. 3.5e-24;
  Matches   54;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          2 NWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMNV 59
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Qy         60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
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RESULT 15
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              |:| |||:||| ||  : |: ||  |::     ||  |||| |    ||||| |:| : |
Db        263 SDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 318

Qy         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db        319 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 366


RESULT 11
US-08-283-971-1
; Sequence 1, Application US/08283971
; Patent No. 5529775
;  GENERAL INFORMATION:
;    APPLICANT:  Ardelt Ph.D, Wojciech J.
;    APPLICANT:  Mikulski, Stanislaw M.
;    TITLE OF INVENTION:  PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mark H. Jay, P.C.
;      STREET:  P.O. Box 020083, General Post Office
;      CITY:  Brooklyn
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  11202-0002
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/283,971
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/921,180
;      FILING DATE:  30-JUL-1992
;      APPLICATION NUMBER:  US 07/178,118
;      FILING DATE:  06-APR-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/436,141
;      FILING DATE:  13-NOV-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jay, Mark H.
;      REGISTRATION NUMBER:  27507
;      REFERENCE/DOCKET NUMBER:  5006 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  718-625-0399
;      TELEFAX:  718-625-0399
;      TELEX:  No. 5529775 Applicable
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  104 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  N
;    ANTI-SENSE:  N
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  Rana pipiens
;      DEVELOPMENTAL STAGE:  Embryo
US-08-283-971-1

  Query Match             45.3%;  Score 272.5;  DB 1;  Length 104;
  Best Local Similarity   49.1%;  Pred. No. 3.5e-24;
  Matches   54;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          2 NWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMNV 59
              :| |||:||| ||  : |: ||  |::     ||  |||| |    ||||| |:| : ||
Db          2 DWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV 57

Qy         60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              |:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         58 LTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104


RESULT 12
US-07-921-619-1
; Sequence 1, Application US/07921619
; Patent No. 5595734
;  GENERAL INFORMATION:
;    APPLICANT:  Ardelt Ph.D, Wojciech J.
;    APPLICANT:  Mikulski, Stanislaw M.
;    TITLE OF INVENTION:  PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mark H. Jay, P.C.
;      STREET:  P.O. Box 020083, General Post Office
;      CITY:  Brooklyn
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  11202-0002
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/921,619
;      FILING DATE:  19920728
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/178,118
;      FILING DATE:  06-APR-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/436,141
;      FILING DATE:  13-NOV-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jay, Mark H.
;      REGISTRATION NUMBER:  27507
;      REFERENCE/DOCKET NUMBER:  5005 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  718-625-0399
;      TELEFAX:  718-625-0399
;      TELEX:  No. 5595734 Applicable
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  104 amino acids
;      TYPE:  AMINO ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  N
;    ANTI-SENSE:  N
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  Rana pipiens
;      DEVELOPMENTAL STAGE:  Embryo
US-07-921-619-1

  Query Match             45.3%;  Score 272.5;  DB 1;  Length 104;
  Best Local Similarity   49.1%;  Pred. No. 3.5e-24;
  Matches   54;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          2 NWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMNV 59
              :| |||:||| ||  : |: ||  |::     ||  |||| |    ||||| |:| : ||
Db          2 DWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV 57

Qy         60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              |:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         58 LTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
```

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;      FILING DATE:  21-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Faris, Susan K.
;      REGISTRATION NUMBER:  41,739
;      REFERENCE/DOCKET NUMBER:  015280-244100US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  57:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  355 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-875-811-57

  Query Match             46.0%;  Score 276.5;  DB 3;  Length 355;
  Best Local Similarity   49.5%;  Pred. No. 5.4e-24;
  Matches   55;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          1 SNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 58
              |:| |||:||| ||  : |: ||  |::     ||  |||| |    ||||| |:| : |
Db          2 SDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 57

Qy         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         58 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 105


RESULT 9
US-08-875-811-64
; Sequence 64, Application US/08875811
; Patent No. 6045793
;  GENERAL INFORMATION:
;    APPLICANT:  Rybak, Susanna M.
;    APPLICANT:  Newton, Dianne L.
;    APPLICANT:  Boque, Lluis
;    APPLICANT:  Wlodawer, Alexander
;    TITLE OF INVENTION:  Recombinant Ribonuclease Proteins
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/875,811
;      FILING DATE:  19-FEB-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/02588
;      FILING DATE:  19-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/011,800
;      FILING DATE:  21-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Faris, Susan K.
;      REGISTRATION NUMBER:  41,739
;      REFERENCE/DOCKET NUMBER:  015280-244100US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  64:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  355 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  Protein
;      LOCATION:  1..355
;      OTHER INFORMATION:  /note= "E6FB[Met-(-1)]SerrOnc"
US-08-875-811-64

  Query Match             46.0%;  Score 276.5;  DB 3;  Length 355;
  Best Local Similarity   49.5%;  Pred. No. 5.4e-24;
  Matches   55;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          1 SNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 58
              |:| |||:||| ||  : |: ||  |::     ||  |||| |    ||||| |:| : |
Db        252 SDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 307

Qy         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db        308 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 355


RESULT 10
US-08-875-811-55
; Sequence 55, Application US/08875811
; Patent No. 6045793
;  GENERAL INFORMATION:
;    APPLICANT:  Rybak, Susanna M.
;    APPLICANT:  Newton, Dianne L.
;    APPLICANT:  Boque, Lluis
;    APPLICANT:  Wlodawer, Alexander
;    TITLE OF INVENTION:  Recombinant Ribonuclease Proteins
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/875,811
;      FILING DATE:  19-FEB-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/02588
;      FILING DATE:  19-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/011,800
;      FILING DATE:  21-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Faris, Susan K.
;      REGISTRATION NUMBER:  41,739
;      REFERENCE/DOCKET NUMBER:  015280-244100US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  55:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  366 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-875-811-55

  Query Match             46.0%;  Score 276.5;  DB 3;  Length 366;
  Best Local Similarity   49.5%;  Pred. No. 5.6e-24;
  Matches   55;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;
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```
;    APPLICANT:  Wlodawer, Alexander
;    TITLE OF INVENTION:  Recombinant Ribonuclease Proteins
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/875,811
;      FILING DATE:  19-FEB-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/02588
;      FILING DATE:  19-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/011,800
;      FILING DATE:  21-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Faris, Susan K.
;      REGISTRATION NUMBER:  41,739
;      REFERENCE/DOCKET NUMBER:  015280-244100US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  61:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  254 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-875-811-61

  Query Match             46.0%;  Score 276.5;  DB 3;  Length 254;
  Best Local Similarity   49.5%;  Pred. No. 3.6e-24;
  Matches   55;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          1 SNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 58
              |:| |||:||| ||  : |: ||  |::     ||  |||| |    |||| |:| : |
Db          2 SDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 57

Qy         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         58 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 105


RESULT 7
US-08-875-811-49
; Sequence 49, Application US/08875811
; Patent No. 6045793
;  GENERAL INFORMATION:
;    APPLICANT:  Rybak, Susanna M.
;    APPLICANT:  Newton, Dianne L.
;    APPLICANT:  Boque, Lluis
;    APPLICANT:  Wlodawer, Alexander
;    TITLE OF INVENTION:  Recombinant Ribonuclease Proteins
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/875,811
;      FILING DATE:  19-FEB-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/02588
;      FILING DATE:  19-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/011,800
;      FILING DATE:  21-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Faris, Susan K.
;      REGISTRATION NUMBER:  41,739
;      REFERENCE/DOCKET NUMBER:  015280-244100US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  49:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  355 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-875-811-49

  Query Match             46.0%;  Score 276.5;  DB 3;  Length 355;
  Best Local Similarity   49.5%;  Pred. No. 5.4e-24;
  Matches   55;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          1 SNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 58
              |:| |||:||| ||  : |: ||  |::     ||  |||| |    |||| |:| : |
Db        252 SDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 307

Qy         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db        308 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 355


RESULT 8
US-08-875-811-57
; Sequence 57, Application US/08875811
; Patent No. 6045793
;  GENERAL INFORMATION:
;    APPLICANT:  Rybak, Susanna M.
;    APPLICANT:  Newton, Dianne L.
;    APPLICANT:  Boque, Lluis
;    APPLICANT:  Wlodawer, Alexander
;    TITLE OF INVENTION:  Recombinant Ribonuclease Proteins
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/875,811
;      FILING DATE:  19-FEB-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/02588
;      FILING DATE:  19-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/011,800
```

```
;      DEVELOPMENTAL STAGE:  Oocyte
US-08-467-955-2

  Query Match             47.0%;  Score 282.5;  DB 1;  Length 104;
  Best Local Similarity   50.0%;  Pred. No. 2.4e-25;
  Matches   55;  Conservative   15;  Mismatches   31;  Indels    9;  Gaps    4;

Qy          2 NWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMNV 59
              :| |||:||: ||  : || ||  |::     ||  |||| |    ||||| |:| : ||
Db          2 DWLTFQKKHVTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV 57

Qy         60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              |:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:||| 
Db         58 LTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGRC 104


RESULT 4
US-08-875-811-32
; Sequence 32, Application US/08875811
; Patent No. 6045793
;  GENERAL INFORMATION:
;    APPLICANT:  Rybak, Susanna M.
;    APPLICANT:  Newton, Dianne L.
;    APPLICANT:  Boque, Lluis
;    APPLICANT:  Wlodawer, Alexander
;    TITLE OF INVENTION:  Recombinant Ribonuclease Proteins
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/875,811
;      FILING DATE:  19-FEB-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/02588
;      FILING DATE:  19-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/011,800
;      FILING DATE:  21-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Faris, Susan K.
;      REGISTRATION NUMBER:  41,739
;      REFERENCE/DOCKET NUMBER:  015280-244100US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  112 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-875-811-32

  Query Match             46.0%;  Score 276.5;  DB 3;  Length 112;
  Best Local Similarity   49.5%;  Pred. No. 1.3e-24;
  Matches   55;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          1 SNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 58
              |:| |||:||| ||  : |: ||  |::     ||  |||| |    ||||| |:| : |
Db          9 SDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 64

Qy         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         65 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 112


RESULT 5
US-08-875-811-59
; Sequence 59, Application US/08875811
; Patent No. 6045793
;  GENERAL INFORMATION:
;    APPLICANT:  Rybak, Susanna M.
;    APPLICANT:  Newton, Dianne L.
;    APPLICANT:  Boque, Lluis
;    APPLICANT:  Wlodawer, Alexander
;    TITLE OF INVENTION:  Recombinant Ribonuclease Proteins
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/875,811
;      FILING DATE:  19-FEB-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/02588
;      FILING DATE:  19-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/011,800
;      FILING DATE:  21-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Faris, Susan K.
;      REGISTRATION NUMBER:  41,739
;      REFERENCE/DOCKET NUMBER:  015280-244100US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  59:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  251 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-875-811-59

  Query Match             46.0%;  Score 276.5;  DB 3;  Length 251;
  Best Local Similarity   49.5%;  Pred. No. 3.5e-24;
  Matches   55;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

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Qy         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
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RESULT 6
US-08-875-811-61
; Sequence 61, Application US/08875811
; Patent No. 6045793
;  GENERAL INFORMATION:
;    APPLICANT:  Rybak, Susanna M.
;    APPLICANT:  Newton, Dianne L.
;    APPLICANT:  Boque, Lluis
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;       STRANDEDNESS:
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
;     FEATURE:
;       NAME/KEY:  Protein
;       LOCATION:  1..111
;       OTHER INFORMATION:  /note= "Frog Lectin from Rana
;       OTHER INFORMATION:  catesbeiana"
US-08-891-848-12

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  Best Local Similarity   99.1%;  Pred. No. 1.9e-60;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

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Qy         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
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Db         62 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111


RESULT 2
US-08-875-811-8
; Sequence 8, Application US/08875811
; Patent No. 6045793
;  GENERAL INFORMATION:
;    APPLICANT:  Rybak, Susanna M.
;    APPLICANT:  Newton, Dianne L.
;    APPLICANT:  Boque, Lluis
;    APPLICANT:  Wlodawer, Alexander
;    TITLE OF INVENTION:  Recombinant Ribonuclease Proteins
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/875,811
;      FILING DATE:  19-FEB-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/02588
;      FILING DATE:  19-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/011,800
;      FILING DATE:  21-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Faris, Susan K.
;      REGISTRATION NUMBER:  41,739
;      REFERENCE/DOCKET NUMBER:  015280-244100US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  111 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  Protein
;      LOCATION:  1..111
;      OTHER INFORMATION:  /note= "Frog Lectin from Rana
;      OTHER INFORMATION:  catesbeiana"
US-08-875-811-8

  Query Match             97.6%;  Score 586.5;  DB 3;  Length 111;
  Best Local Similarity   99.1%;  Pred. No. 1.9e-60;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          2 NWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 60
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Db          2 NWATFQQKHIINTPIINCNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 61

Qy         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
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Db         62 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111


RESULT 3
US-08-467-955-2
; Sequence 2, Application US/08467955
; Patent No. 5728805
;  GENERAL INFORMATION:
;    APPLICANT:  Ardelt Ph.D, Wojciech J.
;    TITLE OF INVENTION:  PHARMACEUTICALS AND METHOD FOR MAKING THEM
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mark H. Jay, P.A.
;      STREET:  P.O. Box E
;      CITY:  Short Hills
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07078-0383
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/467,955
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/178,118
;      FILING DATE:  06-APR-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/436,141
;      FILING DATE:  13-NOV-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/814,332
;      FILING DATE:  03-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/283,970
;      FILING DATE:  01-AUG-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jay, Mark H.
;      REGISTRATION NUMBER:  27507
;      REFERENCE/DOCKET NUMBER:  5007 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-912-9066
;      TELEFAX:  201-912-0442
;      TELEX:  No. 5728805 Applicable
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  104 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  N
;    ANTI-SENSE:  N
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  Rana pipiens
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 11, 2004, 14:33:03 ; Search time 16.4253 Seconds
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Title: US-09-961-400-24
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Sequence: 1 SNWATFQQKHIINTPIICNT.....ICVKCENQYPVHFAGIGRCP 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	586.5	97.6	111	2	US-08-891-848-12	Sequence 12, Appl
2	586.5	97.6	111	3	US-08-875-811-8	Sequence 8, Appli
3	282.5	47.0	104	1	US-08-467-955-2	Sequence 2, Appli
4	276.5	46.0	112	3	US-08-875-811-32	Sequence 32, Appl
5	276.5	46.0	251	3	US-08-875-811-59	Sequence 59, Appl
6	276.5	46.0	254	3	US-08-875-811-61	Sequence 61, Appl
7	276.5	46.0	355	3	US-08-875-811-49	Sequence 49, Appl
8	276.5	46.0	355	3	US-08-875-811-57	Sequence 57, Appl
9	276.5	46.0	355	3	US-08-875-811-64	Sequence 64, Appl
10	276.5	46.0	366	3	US-08-875-811-55	Sequence 55, Appl
11	272.5	45.3	104	1	US-08-283-971-1	Sequence 1, Appli
12	272.5	45.3	104	1	US-07-921-619-1	Sequence 1, Appli
13	272.5	45.3	104	1	US-08-467-955-1	Sequence 1, Appli
14	272.5	45.3	104	2	US-08-891-848-13	Sequence 13, Appl
15	272.5	45.3	104	3	US-08-875-811-1	Sequence 1, Appli
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25	272.5	45.3	129	3	US-08-875-811-63	Sequence 63, Appl
26	272.5	45.3	355	3	US-08-875-811-41	Sequence 41, Appl
27	272.5	45.3	358	3	US-08-875-811-51	Sequence 51, Appl
28	272.5	45.3	379	3	US-08-875-811-43	Sequence 43, Appl
29	271.5	45.2	105	3	US-08-875-811-26	Sequence 26, Appl
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33	267.5	44.5	104	4	US-09-687-748-2	Sequence 2, Appli
34	267.5	44.5	105	3	US-08-875-811-24	Sequence 24, Appl
35	267.5	44.5	358	3	US-08-875-811-45	Sequence 45, Appl
36	267.5	44.5	365	3	US-08-875-811-53	Sequence 53, Appl
37	253.5	42.2	107	3	US-08-875-811-20	Sequence 20, Appl
38	239.5	39.9	111	3	US-08-875-811-22	Sequence 22, Appl
39	235	39.1	114	3	US-09-223-118-3	Sequence 3, Appli
40	231.5	38.5	360	3	US-08-875-811-47	Sequence 47, Appl
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43	224	37.3	114	3	US-09-223-118-4	Sequence 4, Appli
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45	206	34.3	83	4	US-09-071-672-3	Sequence 3, Appli

ALIGNMENTS

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RESULT 1
US-08-891-848-12
; Sequence 12, Application US/08891848
; Patent No. 5955073
;  GENERAL INFORMATION:
;    APPLICANT:  Rybak, Susanna M.
;    APPLICANT:  Youle, Richard J.
;    APPLICANT:  Newton, Dianne L.
;    APPLICANT:  Nicholls, Peter J.
;    TITLE OF INVENTION:  Selective RNase Cytotoxic Reagents
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/891,848
;      FILING DATE:  No. 5955073 yet assigned
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/125,462
;      FILING DATE:  22-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/014,082
;      FILING DATE:  04-FEB-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/779,195
;      FILING DATE:  22-OCT-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/510,696
;      FILING DATE:  20-APR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Weber, Ellen Lauver
;      REGISTRATION NUMBER:  32,762
;      REFERENCE/DOCKET NUMBER:  015280-110310US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  111 amino acids
;      TYPE:  amino acid
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DE   Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.
OX   NCBI_TaxID=8517;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Pancreas;
RX   MEDLINE=94139745; PubMed=8307028;
RA   Zhao W., Beintema J.J., Hofsteenge J.;
RT   "The amino acid sequence of iguana (Iguana iguana) pancreatic
RT   ribonuclease.";
RL   Eur. J. Biochem. 219:641-646(1994).
CC   -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC       phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC       with 2',3'-cyclic phosphate intermediates.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Pancreas.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR   PIR; S41111; S41111.
DR   HSSP; P00656; 1LSQ.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Pyrrolidone carboxylic acid.
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FT   DISULFID     25     80       BY SIMILARITY.
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FT   ACT_SITE     40     40       BY SIMILARITY.
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Search completed: May 11, 2004, 14:35:04
Job time : 9.95475 secs
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DE   Ribonuclease, brain (EC 3.1.27.-) (BRB).
GN   BRN.
OS   Giraffa camelopardalis (Giraffe).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Giraffoidea;
OC   Giraffidae; Giraffa.
OX   NCBI_TaxID=9894;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96139017; PubMed=8587129;
RA   Confalone E., Beintema J.J., Sasso M.P., Carsana A., Palmieri M.,
RA   Vento M.T., Furia A.;
RT   "Molecular evolution of genes encoding ribonucleases in ruminant
RT   species.";
RL   J. Mol. Evol. 41:850-858(1995).
RN   [2]
RP   SEQUENCE OF 31-114 FROM N.A.
RX   MEDLINE=93367815; PubMed=8360916;
RA   Breukelman H.J., Beintema J.J., Confalone E., Costanzo C., Sasso M.P.,
RA   Carsana A., Palmieri M., Furia A.;
RT   "Sequences related to the ox pancreatic ribonuclease coding region in
RT   the genomic DNA of mammalian species.";
RL   J. Mol. Evol. 37:29-35(1993).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S81743; AAB36137.1; -.
DR   EMBL; S65126; AAB27931.1; -.
DR   HSSP; P00656; 2RNS.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT   ACT_SITE     41     41       BY SIMILARITY.
FT   DISULFID     26     84       BY SIMILARITY.
FT   DISULFID     40     95       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID     65     72       BY SIMILARITY.
FT   CARBOHYD     62     62       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   CARBOHYD    129    129       O-LINKED (BY SIMILARITY).
SQ   SEQUENCE   141 AA;  15592 MW;  73745EFE9079591F CRC64;

  Query Match             21.2%;  Score 127.5;  DB 1;  Length 141;
  Best Local Similarity   30.6%;  Pred. No. 7.8e-07;
  Matches   37;  Conservative   17;  Mismatches   44;  Indels   23;  Gaps    7;

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Qy         58 NVL----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHFA 104
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Qy        105 G 105
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Db        122 G 122


RESULT 14
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AC   P87350;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Ribonuclease, brain (EC 3.1.27.-) (BRB).
GN   BRN.
OS   Axis porcinus (Hog deer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC   Cervidae; Cervinae; Axis.
OX   NCBI_TaxID=57737;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98278842; PubMed=9611269;
RA   Breukelman H.J., van der Munnik N., Kleineidam R.G., Furia A.,
RA   Beintema J.J.;
RT   "Secretory ribonuclease genes and pseudogenes in true ruminants.";
RL   Gene 212:259-268(1998).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y11670; CAA72368.1; -.
DR   HSSP; P00656; 1SRN.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT   ACT_SITE     41     41       BY SIMILARITY.
FT   DISULFID     26     84       BY SIMILARITY.
FT   DISULFID     40     95       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID     65     72       BY SIMILARITY.
FT   CARBOHYD     62     62       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   CARBOHYD    129    129       O-LINKED (BY SIMILARITY).
FT   CARBOHYD    133    133       O-LINKED (BY SIMILARITY).
SQ   SEQUENCE   151 AA;  16819 MW;  E95F3757FFC5B233 CRC64;

  Query Match             21.2%;  Score 127.5;  DB 1;  Length 151;
  Best Local Similarity   30.6%;  Pred. No. 8.4e-07;
  Matches   37;  Conservative   17;  Mismatches   44;  Indels   23;  Gaps    7;

Qy          4 ATFQQKHI------INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINM 57
              | |:::|:       :    || :|     :  |:|| ||||:  |   |||:|:
Db          6 AKFRRQHMDAGSSSSGNSNYCNQMMKRR-RMTHGRCKPVNTFVHESLDSVKAVCS---QK 61

Qy         58 NVL----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHFA 104
              |:          | :   :  |  |  :  | | | :  :  || | || | | ||||
Db         62 NITCKNGQPNCYQSNSTMNITDCRETGSSKYPNCAYKTSQKQKYITVACEGNPYVPVHFD 121

Qy        105 G 105
              |
Db        122 G 122


RESULT 15
RNP_IGUIG
ID   RNP_IGUIG      STANDARD;      PRT;   119 AA.
AC   P80287;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
```

```
SQ   SEQUENCE   124 AA;  13804 MW;  0AC28CDE14111845 CRC64;

  Query Match             22.0%;  Score 132.5;  DB 1;  Length 124;
  Best Local Similarity   31.6%;  Pred. No. 2e-07;
  Matches   36;  Conservative   19;  Mismatches   42;  Indels   17;  Gaps    6;

Qy          6 FQQKHI------INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGV-INMN 58
              ||::|:      |:   || :|     :  |:|| ||||:  |   |:|:|: : :|
Db          8 FQRQHMDPDSSSSNSSNYCNLMMSRR-NMTQGRCKPVNTFVHESLADVQAVCSQINVNCK 66

Qy         59 VLSTTRFQLNT------CTRTSITPRP-CPYSSRTETNYICVKCENQ--YPVHF 103
                |  :| |:      | :|  :  | | | :  |  :| | ||     ||||
Db         67 NGQTNCYQSNSTMHITDCRQTGSSKYPNCAYKASQEQKHIIVACEGNPPVPVHF 120


RESULT 11
RNBR_CAPCA
ID   RNBR_CAPCA     STANDARD;      PRT;   151 AA.
AC   P79351;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Ribonuclease, brain (EC 3.1.27.-) (BRB).
OS   Capreolus capreolus (Roe deer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC   Cervidae; Odocoileinae; Capreolus.
OX   NCBI_TaxID=9858;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98278842; PubMed=9611269;
RA   Breukelman H.J., van der Munnik N., Kleineidam R.G., Furia A.,
RA   Beintema J.J.;
RT   "Secretory ribonuclease genes and pseudogenes in true ruminants.";
RL   Gene 212:259-268(1998).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; Y11673; CAA72371.1; -.
DR   HSSP; P00656; 1SRN.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT   ACT_SITE     41     41       BY SIMILARITY.
FT   DISULFID     26     84       BY SIMILARITY.
FT   DISULFID     40     95       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID     65     72       BY SIMILARITY.
FT   CARBOHYD     62     62       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   CARBOHYD    129    129       O-LINKED (BY SIMILARITY).
FT   CARBOHYD    133    133       O-LINKED (BY SIMILARITY).
SQ   SEQUENCE   151 AA;  16971 MW;  392D0E6302F006A6 CRC64;

  Query Match             21.4%;  Score 128.5;  DB 1;  Length 151;
  Best Local Similarity   29.4%;  Pred. No. 6.5e-07;
  Matches   35;  Conservative   17;  Mismatches   44;  Indels   23;  Gaps    6;

Qy          4 ATFQQKHI------INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINM 57
              | |:::|:         |  || :|     :  |:|| ||||:  |   |||:|:
Db          6 AKFRRQHMDSGSSSSGNPNYCNQMMKRR-RMTHGRCKPVNTFVHESLDNVKAVCS---QK 61

Qy         58 NVL----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCENQ--YPVHF 103
              |:           | :   :  | :|  :  | | | :  || | ||     ||||
Db         62 NITCKNGQPNCYQSNSTMNITDCRQTGSSKYPNCAYKTSQKQKYITVACEGDPYVPVHF 120


RESULT 12
ANG2_BOVIN
ID   ANG2_BOVIN     STANDARD;      PRT;   123 AA.
AC   P80929;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Angiogenin-2 (EC 3.1.27.-).
GN   ANG2.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Milk, and Serum;
RX   MEDLINE=97409980; PubMed=9266695;
RA   Strydom D.J., Bond M.D., Vallee B.L.;
RT   "An angiogenic protein from bovine serum and milk -- purification and
RT   primary structure of angiogenin-2.";
RL   Eur. J. Biochem. 247:535-544(1997).
CC   -!- FUNCTION: Binds tightly to placental ribonuclease inhibitor and
CC       has very low ribonuclease activity. Has potent angiogenic
CC       activity. Angiogenin induces vascularization of normal and
CC       malignant tissues. Abolishes protein synthesis by specifically
CC       hydrolyzing cellular tRNAs.
CC   -!- TISSUE SPECIFICITY: Serum and milk.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR   HSSP; P10152; 1AGI.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Angiogenesis;
KW   Protein synthesis inhibitor; Glycoprotein;
KW   Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   ACT_SITE     12     12       BY SIMILARITY.
FT   ACT_SITE     39     39       BY SIMILARITY.
FT   ACT_SITE    113    113       BY SIMILARITY.
FT   DISULFID     25     80
FT   DISULFID     38     91
FT   DISULFID     56    106
FT   CARBOHYD     33     33       N-LINKED (GLCNAC. . .).
SQ   SEQUENCE   123 AA;  14522 MW;  B703B9839919FD2F CRC64;

  Query Match             21.2%;  Score 127.5;  DB 1;  Length 123;
  Best Local Similarity   30.6%;  Pred. No. 6.8e-07;
  Matches   33;  Conservative   19;  Mismatches   43;  Indels   13;  Gaps    5;

Qy          6 FQQKHIINTPI-----ICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAIC---TGVINM 57
              | :||   :|       |||:|:     :   ||  ||||  ::  ::|:|    |
Db          8 FLRKHYDPSPTGHDDRYCNTMMERR--NMTRPCKDTNTFIHGNSDDIRAVCDDRNGEPYR 65

Qy         58 NVLSTTR--FQLNTCTRTSITPR-PCPYSSRTETNYICVKCENQYPVH 102
              | |  :|  ||: ||      :|| || | :       | ::| : :|:|
Db         66 NGLRRSRSPFQVTTCRHRGGSPRPPCRYRAFRANRVIVIRCRDGFPIH 113


RESULT 13
RNBR_GIRCA
ID   RNBR_GIRCA     STANDARD;      PRT;   141 AA.
AC   Q29542; Q29533;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
```

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DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ribonuclease, brain precursor (EC 3.1.27.-) (BRB).
GN   BRN.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92093604; PubMed=1754384;
RA   Sasso M.P., Carsana A., Confalone E., Cosi C., Sorrentino S.,
RA   Viola M., Palmieri M., Russo E., Furia A.;
RT   "Molecular cloning of the gene encoding the bovine brain ribonuclease
RT   and its expression in different regions of the brain.";
RL   Nucleic Acids Res. 19:6469-6474(1991).
RN   [2]
RP   SEQUENCE OF 27-167, AND CARBOHYDRATE-LINKAGE SITES.
RC   TISSUE=Brain;
RX   MEDLINE=89214015; PubMed=3243767;
RA   Watanabe H., Katoh H., Ishii M., Komoda Y., Sanda A., Takizawa Y.,
RA   Ohgi K., Irie M.;
RT   "Primary structure of a ribonuclease from bovine brain.";
RL   J. Biochem. 104:939-945(1988).
RN   [3]
RP   SEQUENCE OF 27-167 FROM N.A.
RX   MEDLINE=96139017; PubMed=8587129;
RA   Confalone E., Beintema J.J., Sasso M.P., Carsana A., Palmieri M.,
RA   Vento M.T., Furia A.;
RT   "Molecular evolution of genes encoding ribonucleases in ruminant
RT   species.";
RL   J. Mol. Evol. 41:850-858(1995)..
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC   ----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X59767; CAA42439.1; -.
DR   EMBL; S81744; AAB36138.1; -.
DR   PIR; S20066; S20066.
DR   HSSP; P00656; 2RNS.
DR   GlycoSuiteDB; P39873; -.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Glycoprotein; Signal.
FT   SIGNAL       1     26
FT   CHAIN       27    167       RIBONUCLEASE, BRAIN.
FT   ACT_SITE    38     38       BY SIMILARITY.
FT   ACT_SITE    67     67       BY SIMILARITY.
FT   ACT_SITE   145    145       BY SIMILARITY.
FT   DISULFID    52    110       BY SIMILARITY.
FT   DISULFID    66    121       BY SIMILARITY.
FT   DISULFID    84    136       BY SIMILARITY.
FT   DISULFID    91     98       BY SIMILARITY.
FT   CARBOHYD    88     88       N-LINKED (GLCNAC. . .).
FT                               /FTId=CAR_000005.
FT   CARBOHYD   155    155       O-LINKED.
FT   CARBOHYD   159    159       O-LINKED.
FT   CONFLICT   155    155       T -> S (IN REF. 2).
SQ   SEQUENCE   167 AA;  18450 MW;  681CAAC3CC2FC459 CRC64;

  Query Match             22.2%;  Score 133.5;  DB 1;  Length 167;
  Best Local Similarity   31.4%;  Pred. No. 2.1e-07;

  Matches   38;  Conservative   17;  Mismatches   43;  Indels   23;  Gaps    7;

Qy          4 ATFQQKHI------INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINM 57
              | |:::|:       : |  || :|     :  |:|| ||||:  |   |||:|:
Db         32 AKFRRQHMDSGSSSSSNPNYCNQMMKRR-RMTHGRCKPVNTFVHESLDDVKAVCS---QK 87

Qy         58 NVL----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHFA 104
              |:           | :  :  |  | :  | | | :  :  || | || | | ||||
Db         88 NITCKNGHPNCYQSKSTMSITDCRETGSSKYPNCAYKTSQKQKYITVACEGNPYVPVHFD 147

Qy        105 G 105
              |
Db        148 G 148


RESULT 10
RNP_PIG
ID   RNP_PIG        STANDARD;      PRT;   124 AA.
AC   P00671;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
GN   RNASE1 OR RNS1.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=70104197; PubMed=5460946;
RA   Jackson R.L., Hirs C.H.W.;
RT   "The primary structure of porcine pancreatic ribonuclease. II. The
RT   amino acid sequence of the reduced S-aminoethylated protein.";
RL   J. Biol. Chem. 245:637-653(1970).
RN   [2]
RP   REVISION TO 2.
RA   Wierenga R.K., Huizinga J.D., Gaastra W., Welling G.W., Beintema J.J.;
RT   "Affinity chromatography of porcine pancreatic ribonuclease and
RT   reinvestigation of the N-terminal amino acid sequence.";
RL   FEBS Lett. 31:181-185(1973).
RN   [3]
RP   DISULFIDE BONDS.
RX   MEDLINE=70104198; PubMed=4904878;
RA   Phelan J.J., Hirs C.H.W.;
RT   "The primary structure of porcine pancreatic ribonuclease. 3. The
RT   disulfide bonds.";
RL   J. Biol. Chem. 245:654-661(1970).
CC   -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC       phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC       with 2',3'-cyclic phosphate intermediates.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Pancreas.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR   PIR; A92071; NRPG.
DR   HSSP; P00656; 1SRN.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT   DISULFID     26     84
FT   DISULFID     40     95
FT   DISULFID     58    110
FT   DISULFID     65     72
FT   ACT_SITE     12     12       BY SIMILARITY.
FT   ACT_SITE     41     41       BY SIMILARITY.
FT   ACT_SITE    119    119       BY SIMILARITY.
FT   CARBOHYD     21     21       N-LINKED (GLCNAC. . .).
FT   CARBOHYD     34     34       N-LINKED (GLCNAC. . .).
FT   CARBOHYD     76     76       N-LINKED (GLCNAC. . .).
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DR   PIR; A00818; NRWHK.
DR   HSSP; P00656; 1SRN.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT   DISULFID     26     84       BY SIMILARITY.
FT   DISULFID     40     95       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID     65     72       BY SIMILARITY.
FT   ACT_SITE     12     12       BY SIMILARITY.
FT   ACT_SITE     41     41       BY SIMILARITY.
FT   ACT_SITE    119    119       BY SIMILARITY.
FT   CARBOHYD     76     76       N-LINKED (GLCNAC. . .) (30%).
SQ   SEQUENCE   124 AA;  14125 MW;  F57475459F697E20 CRC64;

  Query Match             22.5%;  Score 135.5;  DB 1;  Length 124;
  Best Local Similarity   33.3%;  Pred. No. 9.4e-08;
  Matches   39;  Conservative   16;  Mismatches   39;  Indels   23;  Gaps    7;

Qy          6 FQQKHII------NTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 59
              ||::|:      | |  || :|     :  |:|| ||||:  |   |||:|:     ||
Db          8 FQRQHMDSGNSPGNNPNYCNQMMMRR-KMTQGRCKPVNTFVHESLEDVKAVCS---QKNV 63

Qy         60 L----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 103
              |          | :   :  | :|  :  | | | :  :  :| | || | | ||||
Db         64 LCKNGRTNCYESNSTMHITDCRQTGSSKYPNCAYKTSQKEKHIIVACEGNPYVPVHF 120


RESULT 8
ANGI_MOUSE
ID   ANGI_MOUSE     STANDARD;      PRT;   145 AA.
AC   P21570;
DT   01-MAY-1991 (Rel. 18, Created)
DT   01-MAY-1991 (Rel. 18, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).
GN   ANG.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91025023; PubMed=2222458;
RA   Bond M.D., Vallee B.L.;
RT   "Isolation and sequencing of mouse angiogenin DNA.";
RL   Biochem. Biophys. Res. Commun. 171:988-995(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Liver;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   PARTIAL SEQUENCE.
RC   TISSUE=Serum;
RX   MEDLINE=93192291; PubMed=8448182;
RA   Bond M.D., Strydom D.J., Vallee B.L.;
RT   "Characterization and sequencing of rabbit, pig and mouse
RT   angiogenins: discernment of functionally important residues and
RT   regions.";
RL   Biochim. Biophys. Acta 1162:177-186(1993).
CC   -!- FUNCTION: May function as a tRNA-specific ribonuclease that binds
CC       to actin on the surface of endothelial cells; once bound,
CC       angiogenin is endocytosed and translocated to the nucleus, thereby
CC       promoting the endothelial invasiveness necessary for blood vessel
CC       formation. Angiogenin induces vascularization of normal and
CC       malignant tissues. Abolishes protein synthesis by specifically
CC       hydrolyzing cellular tRNAs.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U22516; AAA91366.1; -.
DR   EMBL; BC055355; AAH55355.1; -.
DR   PIR; A35932; A35932.
DR   HSSP; P03950; 1A4Y.
DR   MGD; MGI:88022; Ang.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Angiogenesis;
KW   Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
FT   SIGNAL        1     24
FT   CHAIN        25    145       ANGIOGENIN.
FT   MOD_RES      25     25       PYRROLIDONE CARBOXYLIC ACID (BY
FT                                SIMILARITY).
FT   ACT_SITE     37     37       BY SIMILARITY.
FT   ACT_SITE     64     64       BY SIMILARITY.
FT   ACT_SITE    137    137       BY SIMILARITY.
FT   DISULFID     50    104       BY SIMILARITY.
FT   DISULFID     63    115       BY SIMILARITY.
FT   DISULFID     81    130       BY SIMILARITY.
SQ   SEQUENCE   145 AA;  16228 MW;  06944260BB764938 CRC64;

  Query Match             22.5%;  Score 135.5;  DB 1;  Length 145;
  Best Local Similarity   39.5%;  Pred. No. 1.1e-07;
  Matches   30;  Conservative   12;  Mismatches   29;  Indels    5;  Gaps    3;

Qy         33 CKRVNTFIISSATTVKAIC---TGVINMNV-LSTTRFQLNTCTRTSITPR-PCPYSSRTE 87
              || |||||  : : :||||         |: :| : ||: ||  |  :|| || | :
Db         63 CKDVNTFIHGNKSNIKAICGANGSPYRENLRMSKSPFQVTTCKHTGGSPRPPCQYRASAG 122

Qy         88 TNYICVKCENQYPVHF 103
                :: : |||  ||||
Db        123 FRHVVIACENGLPVHF 138


RESULT 9
RNBR_BOVIN
ID   RNBR_BOVIN     STANDARD;      PRT;   167 AA.
AC   P39873;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
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RT   developmentally regulated genes when expressed in NIH 3T3
RT   fibroblasts.";
RL   Mol. Cell. Biol. 17:1503-1512(1997).
CC   -!- FUNCTION: Angiogenin induces vascularization of normal and
CC       malignant tissues. Abolishes protein synthesis by specifically
CC       hydrolyzing cellular tRNAs (By similarity).
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC   ----------------------------------------------------------------------
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U72672; AAC05794.1; -.
DR   HSSP; P10152; 1AGI.
DR   MGD; MGI:1201793; Angl.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Angiogenesis;
KW   Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
FT   SIGNAL        1     24       POTENTIAL.
FT   CHAIN        25    145       ANGIOGENIN-3.
FT   MOD_RES      25     25       PYRROLIDONE CARBOXYLIC ACID
FT                                (BY SIMILARITY).
FT   ACT_SITE     37     37       BY SIMILARITY.
FT   ACT_SITE     64     64       BY SIMILARITY.
FT   ACT_SITE    137    137       BY SIMILARITY.
FT   DISULFID     50    104       BY SIMILARITY.
FT   DISULFID     63    115       BY SIMILARITY.
FT   DISULFID     81    130       BY SIMILARITY.
SQ   SEQUENCE   145 AA;  16696 MW;  DE9D3BC92F1D682C CRC64;

  Query Match             25.7%;  Score 154.5;  DB 1;  Length 145;
  Best Local Similarity   43.6%;  Pred. No. 1e-09;
  Matches   34;  Conservative   12;  Mismatches   23;  Indels    9;  Gaps    4;

Qy         33 CKRVNTFIISSATTVKAIC------TGVINMNVLSTTRFQLNTCTRTSITPR-PCPYSSR 85
              || |||||  :   :||||       || |  : | :|||: |||    :|| || |::
Db         63 CKEVNTFIHDTKNNIKAICGENGRPYGV-NFRI-SNSRFQVTTCTHKGGSPRPPCQYNAF 120

Qy         86 TETNYICVKCENQYPVHF 103
                :  || : ||: :||||
Db        121 KDFRYIVIACEDGWPVHF 138


RESULT 6
ANGR_MOUSE
ID   ANGR_MOUSE     STANDARD;      PRT;   145 AA.
AC   Q64438;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Angiogenin-related protein precursor.
GN   ANGRP.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129; TISSUE=Liver;
RX   MEDLINE=96079109; PubMed=8530072;
RA   Brown W.E., Nobile V., Subramanian V., Shapiro R.;
RT   "The mouse angiogenin gene family: structures of an angiogenin-related
RT   protein gene and two pseudogenes.";
RL   Genomics 29:200-206(1995).
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC   ----------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U22519; AAA91367.1; -.
DR   HSSP; P03950; 1A4Y.
DR   MGD; MGI:104984; Angrp.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal; Hydrolase; Nuclease; Endonuclease;
KW   Pyrrolidone carboxylic acid.
FT   SIGNAL        1     24       POTENTIAL.
FT   CHAIN        25    145       ANGIOGENIN-RELATED PROTEIN.
FT   MOD_RES      25     25       PYRROLIDONE CARBOXYLIC ACID (BY
FT                                SIMILARITY).
FT   ACT_SITE     37     37       BY SIMILARITY.
FT   ACT_SITE     64     64       BY SIMILARITY.
FT   ACT_SITE    137    137       BY SIMILARITY.
FT   DISULFID     50    104       BY SIMILARITY.
FT   DISULFID     63    115       BY SIMILARITY.
FT   DISULFID     81    130       BY SIMILARITY.
SQ   SEQUENCE   145 AA;  16612 MW;  29A6EB814429C4AD CRC64;

  Query Match             24.9%;  Score 149.5;  DB 1;  Length 145;
  Best Local Similarity   43.4%;  Pred. No. 3.5e-09;
  Matches   33;  Conservative   10;  Mismatches   28;  Indels    5;  Gaps    3;

Qy         33 CKRVNTFIISSATTVKAIC---TGVINMNV-LSTTRFQLNTCTRTSITPR-PCPYSSRTE 87
              || |||||  :   :||||         |: :| :|||: |||    :|| || | :
Db         63 CKDVNTFIHDTKNNIKAICGKKGSPYGRNLRISKSRFQVTTCTHKGRSPRPPCRYRASKG 122

Qy         88 TNYICVKCENQYPVHF 103
                || : ||| :||||
Db        123 FRYIIIGCENGWPVHF 138


RESULT 7
RNP_BALAC
ID   RNP_BALAC      STANDARD;      PRT;   124 AA.
AC   P00673;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
GN   RNASE1 OR RNS1.
OS   Balaenoptera acutorostrata (Minke whale) (Lesser rorqual).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
OC   Balaenopteridae; Balaenoptera.
OX   NCBI_TaxID=9767;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76277855; PubMed=962870;
RA   Emmens M., Welling G.W., Beintema J.J.;
RT   "The amino acid sequence of pike-whale (lesser-rorqual) pancreatic
RT   ribonuclease.";
RL   Biochem. J. 157:317-323(1976).
CC   -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC       phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC       with 2',3'-cyclic phosphate intermediates.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Pancreas.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
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RL   J. Biochem. 106:729-735(1989).
CC   -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC       phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC       with 2',3'-cyclic phosphate intermediates.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR   PIR; JX0085; JX0085.
DR   HSSP; P11916; 1BC4.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   ACT_SITE     10     10       BY SIMILARITY.
FT   ACT_SITE     35     35       BY SIMILARITY.
FT   ACT_SITE    104    104       BY SIMILARITY.
FT   DISULFID     19     72       BY SIMILARITY.
FT   DISULFID     34     82       BY SIMILARITY.
FT   DISULFID     52     97       BY SIMILARITY.
FT   DISULFID     94    111       PROBABLE.
SQ   SEQUENCE   111 AA;  12461 MW;  D64BA72456C10788 CRC64;

  Query Match             61.4%;  Score 369;  DB 1;  Length 111;
  Best Local Similarity   65.5%;  Pred. No. 6.4e-33;
  Matches   72;  Conservative    9;  Mismatches   27;  Indels    2;  Gaps    2;

Qy          2 NWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMNV 59
              ||| |::||| :|  | ||||||  ||||||:||  |||||||   |||||:||  :
Db          2 NWAKFKEKHIRSTSSIDCNTIMDKAIYIVGGKCKERNTFIISSEDNVKAICSGVSPDRKE 61

Qy         60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              |||| |:|||| | |||||||||    : | |||||| | |||| |||:|
Db         62 LSTTSFKLNTCIRDSITPRPCPYHPSPDNNKICVKCEKQLPVHFVGIGKC 111


RESULT 4
RN30_RANPI
ID   RN30_RANPI     STANDARD;      PRT;   104 AA.
AC   P22069;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   P-30 protein (EC 3.1.27.-) (Onconase).
OS   Rana pipiens (Northern leopard frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8404;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Embryo;
RX   MEDLINE=91093131; PubMed=1985896;
RA   Ardelt W., Mikulski S.M., Shogen K.;
RT   "Amino acid sequence of an anti-tumor protein from Rana pipiens
RT   oocytes and early embryos. Homology to pancreatic ribonucleases.";
RL   J. Biol. Chem. 266:245-251(1991).
RN   [2]
RP   3D-STRUCTURE MODELING.
RX   MEDLINE=93066156; PubMed=1438177;
RA   Mosimann S.C., Johns K.L., Ardelt W., Mikulski S.M., Shogen K.,
RA   James M.N.G.;
RT   "Comparative molecular modeling and crystallization of P-30 protein:
RT   a novel antitumor protein of Rana pipiens oocytes and early
RT   embryos.";
RL   Proteins 14:392-400(1992).
RN   [3]
RP   X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
RX   MEDLINE=94166079; PubMed=8120892;
RA   Mosimann S.C., Ardelt W., James M.N.G.;
RT   "Refined 1.7 A X-ray crystallographic structure of P-30 protein, an
RT   amphibian ribonuclease with anti-tumor activity.";
RL   J. Mol. Biol. 236:1141-1153(1994).
CC   -!- FUNCTION: Basic protein with antiproliferative/cytotoxic activity
CC       against several tumor cell lines in vitro, as well as antitumor
CC       in vivo. It exhibits a ribonuclease-like activity against high
CC       molecular weight ribosomal RNA.
CC   -!- DEVELOPMENTAL STAGE: Early embryos (up to four blastomere stage).
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR   PDB; 1ONC; 31-JAN-94.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; 3D-structure;
KW   Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   ACT_SITE     10     10
FT   ACT_SITE     31     31
FT   ACT_SITE     97     97
FT   DISULFID     19     68
FT   DISULFID     30     75
FT   DISULFID     48     90
FT   DISULFID     87    104
FT   HELIX         3     10
FT   STRAND       11     12
FT   HELIX        19     22
FT   TURN         23     24
FT   TURN         26     30
FT   STRAND       33     38
FT   HELIX        41     45
FT   HELIX        46     48
FT   TURN         49     50
FT   STRAND       55     58
FT   STRAND       63     70
FT   TURN         74     75
FT   STRAND       77     84
FT   STRAND       86     91
FT   TURN         92     93
FT   STRAND       94    101
SQ   SEQUENCE   104 AA;  11845 MW;  22A753C2F9E566B4 CRC64;

  Query Match             45.3%;  Score 272.5;  DB 1;  Length 104;
  Best Local Similarity   49.1%;  Pred. No. 1.4e-22;
  Matches   54;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          2 NWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMNV 59
              :| |||:||| ||  : |: ||  |::     ||  |||| |    ||||| |:| : ||
Db          2 DWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV 57

Qy         60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              |:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         58 LTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104


RESULT 5
ANG3_MOUSE
ID   ANG3_MOUSE     STANDARD;      PRT;   145 AA.
AC   P97802;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Angiogenin-3 precursor (EC 3.1.27.-) (Angiogenin-related protein 2)
DE   (EF-5).
GN   ANG3 OR ANGL.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RX   MEDLINE=97184476; PubMed=9032278;
RA   Fu X., Kamps M.P.;
RT   "E2a-Pbx1 induces aberrant expression of tissue-specific and
```

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CC       residues with a 3'flanking guanine. Hydrolyzes poly(U) and poly(C)
CC       as substrates, and prefers the former. The S-lectins in frog eggs
CC       may be involved in the fertilization and development of the frog
CC       embryo. This lectin agglutinates various animal cells, including
CC       normal lymphocytes, erythrocytes, and fibroblasts of animal and
CC       human origin. It is cytotoxic against several tumor cells.
CC   -!- SUBUNIT: Monomer.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF039104; AAD10702.1; -.
DR   PIR; A27121; A27121.
DR   PDB; 1BC4; 28-OCT-98.
DR   PDB; 1M07; 21-JAN-03.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure;
KW   Signal; Pyrrolidone carboxylic acid.
FT   SIGNAL       1     22
FT   CHAIN       23    133       RIBONUCLEASE, OOCYTES.
FT   MOD_RES     23     23       PYRROLIDONE CARBOXYLIC ACID.
FT   ACT_SITE    32     32
FT   ACT_SITE    57     57
FT   ACT_SITE   125    125
FT   DISULFID    41     93
FT   DISULFID    56    103
FT   DISULFID    74    118
FT   DISULFID   115    132
FT   HELIX       25     32
FT   HELIX       41     45
FT   TURN        48     49
FT   STRAND      59     63
FT   HELIX       67     73
FT   TURN        74     74
FT   STRAND      79     84
FT   STRAND      90     95
FT   STRAND     105    110
FT   STRAND     114    119
FT   TURN       120    121
FT   STRAND     122    129
SQ   SEQUENCE   133 AA;  14762 MW;  A7D62594F7D16F0C CRC64;

  Query Match             97.6%;  Score 586.5;  DB 1;  Length 133;
  Best Local Similarity   99.1%;  Pred. No. 3.1e-56;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          2 NWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 60
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db         24 NWATFQQKHIINTPIINCNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 83

Qy         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 133


RESULT 2
LECS_RANJA
ID   LECS_RANJA     STANDARD;      PRT;   111 AA.
AC   P18839;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Sialic acid-binding lectin (EC 3.1.27.-).
OS   Rana japonica (Japanese reddish frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8402;
RN   [1]
RP   SEQUENCE, AND DISULFIDE BONDS.
RC   TISSUE=Egg;
RX   MEDLINE=91035319; PubMed=2229005;
RA   Kamiya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawauchi H.,
RA   Takayanagi Y., Titani K.;
RT   "Amino acid sequence of a lectin from Japanese frog (Rana japonica)
RT   eggs.";
RL   J. Biochem. 108:139-143(1990).
CC   -!- FUNCTION: The S-lectins in frog eggs may be involved in the
CC       fertilization and development of the frog embryo. This lectin
CC       preferentially agglutinate a large variety of tumor cells, but it
CC       does not agglutinate non-transformed cells and erythrocytes.
CC   -!- SUBUNIT: Monomer.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR   PIR; JX0120; JX0120.
DR   HSSP; P11916; 1BC4.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin;
KW   Pyrrolidone carboxylic acid.
FT   MOD_RES      1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   ACT_SITE    10     10       BY SIMILARITY.
FT   ACT_SITE    35     35       BY SIMILARITY.
FT   ACT_SITE   104    104       BY SIMILARITY.
FT   DISULFID    19     72
FT   DISULFID    34     82
FT   DISULFID    52     97
FT   DISULFID    94    111
SQ   SEQUENCE   111 AA;  12326 MW;  FDEBDDF3834ED679 CRC64;

  Query Match             74.9%;  Score 450;  DB 1;  Length 111;
  Best Local Similarity   78.2%;  Pred. No. 1.2e-41;
  Matches   86;  Conservative    7;  Mismatches   15;  Indels    2;  Gaps    2;

Qy          2 NWATFQQKHIINTP-IICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGV-INMNV 59
              ||| ||:||| ||  | |||||| :|||||||||  |||||||||||||||:|   | ||
Db          2 NWAKFQEKHIPNTSNINCNTIMDKSIYIVGGQCKERNTFIISSATTVKAICSGASTNRNV 61

Qy         60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              |||||||||||  |::  ||||||:|||||| ||||||||: ||||||||||
Db         62 LSTTRFQLNTCIRSATAPRPCPYNSRTETNVICVKCENRLPVHFAGIGRC 111


RESULT 3
RNPL_RANCA
ID   RNPL_RANCA     STANDARD;      PRT;   111 AA.
AC   P14626;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Ribonuclease, liver (EC 3.1.27.5).
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Liver;
RX   MEDLINE=90130374; PubMed=2613682;
RA   Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,
RA   Okazaki T., Ohgi K., Irie M.;
RT   "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana)
RT   liver.";
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 11, 2004, 14:24:28 ; Search time 9.95475 Seconds
(without alignments)
575.375 Million cell updates/sec

Title: US-09-961-400-24
Perfect score: 601
Sequence: 1 SNWATFQQKHIINTPIICNT.....ICVKCENQYPVHFAGIGRCP 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	586.5	97.6	133	1	RNPO_RANCA	P11916 rana catesb
2	450	74.9	111	1	LECS_RANJA	P18839 rana japoni
3	369	61.4	111	1	RNPL_RANCA	P14626 rana catesb
4	272.5	45.3	104	1	RN30_RANPI	P22069 rana pipien
5	154.5	25.7	145	1	ANG3_MOUSE	P97802 mus musculu
6	149.5	24.9	145	1	ANGR_MOUSE	Q64438 mus musculu
7	135.5	22.5	124	1	RNP_BALAC	P00673 balaenopter
8	135.5	22.5	145	1	ANGI_MOUSE	P21570 mus musculu
9	133.5	22.2	167	1	RNBR_BOVIN	P39873 bos taurus
10	132.5	22.0	124	1	RNP_PIG	P00671 sus scrofa
11	128.5	21.4	151	1	RNBR_CAPCA	P79351 capreolus c
12	127.5	21.2	123	1	ANG2_BOVIN	P80929 bos taurus
13	127.5	21.2	141	1	RNBR_GIRCA	Q29542 giraffa cam
14	127.5	21.2	151	1	RNBR_AXIPR	P87350 axis porcin
15	126.5	21.0	119	1	RNP_IGUIG	P80287 iguana igua
16	126.5	21.0	146	1	ANGI_CERAE	Q8wn66 cercopithec
17	126.5	21.0	146	1	ANGI_MIOTA	Q8wn65 miopithecus
18	125	20.8	146	1	ANGI_SAISC	Q8wn60 saimiri sci
19	123.5	20.5	143	1	RNBR_SHEEP	Q29543 ovis aries
20	122.5	20.4	124	1	RNP_ANTAM	P00668 antilocapra
21	122	20.3	122	1	RNP_MACRU	P00686 macropus ru
22	120.5	20.0	128	1	RNP_MYOCO	P00676 myocastor c
23	120.5	20.0	147	1	ANGI_PONPY	Q8wn67 pongo pygma
24	120.5	20.0	149	1	RNP_MOUSE	P00683 mus musculu
25	120	20.0	146	1	ANGI_AOTTR	Q8wn61 aotus trivi
26	119.5	19.9	123	1	ANGI_PIG	P31346 sus scrofa
27	118.5	19.7	128	1	RNPB_CAVPO	P00679 cavia porce
28	118	19.6	146	1	ANGI_SAGOE	Q8wn62 saguinus oe
29	117.5	19.6	128	1	RNP_HORSE	P00674 equus cabal
30	116.5	19.4	124	1	RNP_CAMDR	P00670 camelus dro
31	116.5	19.4	128	1	RNP_PROGU	P04059 proechimys
32	115.5	19.2	119	1	RNS4_BOVIN	P15467 bos taurus
33	115.5	19.2	146	1	ANGI_MACMU	Q8wn63 macaca mula
34	114	19.0	148	1	ANGI_BOVIN	P10152 bos taurus
35	113.5	18.9	124	1	RNP_RANTA	P00666 rangifer ta
36	113.5	18.9	125	1	ANGI_RABIT	P31347 oryctolagus
37	113.5	18.9	146	1	ANGI_PAPHA	Q8wn64 papio hamad
38	113	18.8	147	1	ANGI_HUMAN	P03950 homo sapien
39	113	18.8	147	1	ANGI_PANTR	Q8wme8 pan troglod
40	112.5	18.7	124	1	RNP_CAPCA	P00664 capreolus c
41	112.5	18.7	124	1	RNP_GIRCA	P00662 giraffa cam
42	112.5	18.7	148	1	RNS4_MOUSE	Q9jjh1 mus musculu
43	111.5	18.6	130	1	RNP_CRILO	P24717 cricetulus
44	111.5	18.6	147	1	RNS4_RAT	O55004 rattus norv
45	111.5	18.6	149	1	RNP_ACOCA	Q9wtt5 acomys cahi

ALIGNMENTS

RESULT 1
RNPO_RANCA
ID RNPO_RANCA STANDARD; PRT; 133 AA.
AC P11916; Q9PWR7;
DT 01-OCT-1989 (Rel. 12, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ribonuclease, oocytes precursor (EC 3.1.27.-) (RC-RNase) (Sialic acid-
DE binding lectin) (SBL-C).
GN RCR.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98165825; PubMed=9497370;
RA Huang H.C., Wang S.C., Leu Y.J., Lu S.C., Liao Y.D.;
RT "The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease.
RT Tissue distribution, cloning, purification, cytotoxicity, and active
RT residues for RNase activity.";
RL J. Biol. Chem. 273:6395-6401(1998).
RN [2]
RP SEQUENCE OF 23-133.
RC TISSUE=Egg;
RX MEDLINE=87299649; PubMed=3304421;
RA Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H.,
RA Takayanagi G., Hakomori S.;
RT "Amino acid sequence of sialic acid binding lectin from frog (Rana
RT catesbeiana) eggs.";
RL Biochemistry 26:2189-2194(1987).
RN [3]
RP CHARACTERIZATION, AND SEQUENCE OF 81-101.
RX MEDLINE=92220613; PubMed=1373237;
RA Liao Y.-D.;
RT "A pyrimidine-guanine sequence-specific ribonuclease from Rana
RT catesbeiana (bullfrog) oocytes.";
RL Nucleic Acids Res. 20:1371-1377(1992).
RN [4]
RP CHARACTERIZATION.
RC TISSUE=Egg;
RX MEDLINE=93192604; PubMed=8448385;
RA Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawauchi H.,
RA Takayanagi Y., Hakomori S., Titani K.;
RT "Ribonuclease activity of sialic acid-binding lectin from Rana
RT catesbeiana eggs.";
RL Glycobiology 3:37-45(1993).
RN [5]
RP STRUCTURE BY NMR OF 23-133.
RX MEDLINE=98437383; PubMed=9761686;
RA Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;
RT "The solution structure of a cytotoxic ribonuclease from the oocytes
RT of Rana catesbeiana (bullfrog).";
RL J. Mol. Biol. 283:231-244(1998).
CC -!- FUNCTION: Preferentially cleaves single-stranded RNA at pyrimidine

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Qy          33 CKRVNTFIISSATTVKAICTG----VINMNVLSTTRFQLNTCTRTSITPR-PCPYSSRTE 87
               || |||||  :   :||||        |    | : ||: ||     : | || | :
Db          39 CKEVNTFIHGTRNDIKAICNDKNGEPYNNFRRSKSPFQITTCKHKGGSNRPPCGYRATAG 98

Qy          88 TNYICVKCENQYPVHF 103
                 | | |||  ||||
Db          99 FRTIAVACENGLPVHF 114
```

RESULT 15
NRGPB
pancreatic ribonuclease (EC 3.1.27.5) B - guinea pig (tentative sequence)
N;Alternate names: RNase IB
C;Species: Cavia porcellus (guinea pig)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C;Accession: A00826
R;van den Berg, A.; van den Hende-Timmer, L.; Hofsteenge, J.; Gaastra, W.; Beintema, J.J
Eur. J. Biochem. 75, 91-100, 1977
A;Title: Guinea pig pancreatic ribonucleases. Isolation, properties, primary structure a
A;Reference number: A91247; MUID:77185023; PMID:862624
A;Accession: A00826
A;Molecule type: protein
A;Residues: 1-128 <VAN>
A;Note: 64-Pro was also found
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;21,34/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted

Query Match 19.7%; Score 118.5; DB 1; Length 128;
Best Local Similarity 31.6%; Pred. No. 8.6e-05;
Matches 37; Conservative 14; Mismatches 43; Indels 23; Gaps 6;

```
Qy           6 FQQKHI------INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 59
               ||::|:       |:   || :|     :  |:|| ||||:  |   |:|:|      ||
Db           8 FQRQHMDPEGSPSNSSNYCNVMMIRR-NMTQGRCKPVNTFVHESLADVQAVC---FQKNV 63

Qy          60 L----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCENQ--YPVHF 103
               |          | :| ::  |  || :  | | |         | | ||     ||||
Db          64 LCKNGQTNCYQSYSRMRITDCRVTSSSKFPNCSYRMSQAQKSIIVACEGDPYVPVHF 120
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Search completed: May 11, 2004, 14:37:08
Job time : 14.4389 secs

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Db          6 AKFERQHIDSNPSSVSSSNYCNQMMKSR-NLTQGRCKPVNTFVHESLADVQAVCS---QK 61

Qy         58 NVL----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 103
              ||           | :   :  |  |   :  | | | :     :| | || | | |||:
Db         62 NVACKNGQTNCYQSYSTMSITDCRETGSSKYPNCAYKTTQAKKHIIVACEGNPYVPVHY 120


RESULT 11
NRKGR
pancreatic ribonuclease (EC 3.1.27.5) - red kangaroo
N;Alternate names: RNase 1; RNase A
C;Species: Macropus rufus, Megaleia rufa (red kangaroo)
C;Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 04-Oct-1996
C;Accession: A00833
R;Gaastra, W.; Welling, G.W.; Beintema, J.J.
Eur. J. Biochem. 86, 209-217, 1978
A;Title: The amino-acid sequence of kangaroo pancreatic ribonuclease.
A;Reference number: A00833; MUID:78190621; PMID:658039
A;Accession: A00833
A;Molecule type: protein
A;Residues: 1-122 <GAA>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;11,40,117/Active site: His, Lys, His #status predicted
F;25-83,39-94,57-109,64-71/Disulfide bonds: #status predicted
F;61/Binding site: carbohydrate (Asn) (covalent) #status absent

  Query Match             20.3%;  Score 122;  DB 1;  Length 122;
  Best Local Similarity   30.7%;  Pred. No. 3.7e-05;
  Matches   35;  Conservative   16;  Mismatches   45;  Indels   18;  Gaps    6;

Qy          6 FQQKHI------INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAIC-------- 51
              ||::|:        ::   || :|     :  |:|| :||||    : | |:|
Db          7 FQRQHMDTEHSTASSSNYCNLMMKAR-DMTSGRCKPLNTFIHEPKSVVDAVCHQENVTCK 65

Qy         52 TGVINMNVLSTTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCENQY-PVHF 103
               |  |    | :|  :  | :|  :  | | | :      | | || || ||||
Db         66 NGRTNC-YKSNSRLSITNCRQTGASKYPNCQYETSNLNKQIIVACEGQYVPVHF 118


RESULT 12
NRCU
pancreatic ribonuclease (EC 3.1.27.5) - nutria (tentative sequence)
N;Alternate names: RNase 1; RNase A
C;Species: Myocastor coypus (nutria, coypu)
C;Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
C;Accession: A00822
R;van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
Biochim. Biophys. Acta 453, 400-409, 1976
A;Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic
A;Reference number: A90612; MUID:77065676; PMID:999896
A;Accession: A00822
A;Molecule type: protein
A;Residues: 1-128 <VAN>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F;34/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match             20.0%;  Score 120.5;  DB 1;  Length 128;
  Best Local Similarity   31.6%;  Pred. No. 5.4e-05;
  Matches   37;  Conservative   15;  Mismatches   42;  Indels   23;  Gaps    7;

Qy          6 FQQKHI------INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 59
              |:::|:        |  || :| :   :  |:|| ||||:      |:|:|      ||
Db          8 FERQHMDSRGSPSTNPNYCNEMMKSR-NMTQGRCKPVNTFVHEPLADVQAVC---FQKNV 63

Qy         60 L----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 103
              |          | :   :  |  || :  | | | :   |   | | || | | ||||
Db         64 LCKNGQTNCYQSNSNMHITDCRVTSNSDYPNCSYRTSQEEKSIVVACEGNPYVPVHF 120


RESULT 13
NRMS
pancreatic ribonuclease (EC 3.1.27.5) precursor - mouse
N;Alternate names: RNase 1; RNase A
C;Species: Mus musculus (house mouse)
C;Date: 30-Nov-1980 #sequence_revision 13-Mar-1997 #text_change 18-Jun-1999
C;Accession: A34090; S22598; A00830
R;Schueller, C.; Nijssen, H.M.J.; Kok, R.; Beintema, J.J.
Mol. Biol. Evol. 7, 29-44, 1990
A;Title: Evolution of nucleic acids coding for ribonucleases: the mRNA sequence of mouse
A;Reference number: A34090; MUID:90136034; PMID:2299980
A;Accession: A34090
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-149 <SCH>
A;Cross-references: GB:M27814; NID:g200762; PIDN:AAA40060.1; PID:g200763
R;Samuelson, L.C.; Wiebauer, K.; Howard, G.; Schmid, R.M.; Koeplin, D.; Meisler, M.H.
Nucleic Acids Res. 19, 6935-6941, 1991
A;Title: Isolation of the murine ribonuclease gene Rib-1: structure and tissue specific e
A;Reference number: S22598; MUID:92107684; PMID:1840677
A;Accession: S22598
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-149 <SAM>
A;Cross-references: EMBL:X60103; NID:g53981; PIDN:CAA42697.1; PID:g53982
R;Lenstra, J.A.; Beintema, J.J.
Eur. J. Biochem. 98, 399-408, 1979
A;Title: The amino acid sequence of mouse pancreatic ribonuclease.
A;Reference number: A00830; MUID:80024269; PMID:556267
A;Accession: A00830
A;Molecule type: protein
A;Residues: 26-149 <LEN>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-149/Product: pancreatic ribonuclease #status experimental <MAT>
F;37,66,144/Active site: His, Lys, His #status predicted
F;51-109,65-120,83-135,90-97/Disulfide bonds: #status predicted
F;62,87/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             20.0%;  Score 120.5;  DB 1;  Length 149;
  Best Local Similarity   30.8%;  Pred. No. 6.4e-05;
  Matches   36;  Conservative   16;  Mismatches   42;  Indels   23;  Gaps    7;

Qy          6 FQQKHI------INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 59
              ||::|:        ||:|  || :|     :  | || ||||:      |:|:|:     ||
Db         33 FQRQHMDPDGSSINSPTYCNQMMKRR-DMTNGSCKPVNTFVHEPLADVQAVCS---QENV 88

Qy         60 L----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 103
                        |::   :  |     :  | | | :     :| | || | | ||||
Db         89 TCKNRKSNCYKSSSALHITDCHLKGNSKYPNCDYKTTQYQKHIIVACEGNPYVPVHF 145


RESULT 14
A43825
angiogenin - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S29834; A43825
R;Bond, M.D.; Strydom, D.J.; Vallee, B.L.
Biochim. Biophys. Acta 1162, 177-186, 1993
A;Title: Characterization and sequencing of rabbit, pig and mouse angiogenins: discernmer
A;Reference number: S29833; MUID:93192291; PMID:8448182
A;Accession: S29834
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-123 <BON>
A;Note: this sequence was submitted to the Protein Sequence Database, December 1992
C;Superfamily: pancreatic ribonuclease

  Query Match             19.9%;  Score 119.5;  DB 1;  Length 123;
  Best Local Similarity   39.5%;  Pred. No. 6.6e-05;
  Matches   30;  Conservative    6;  Mismatches   35;  Indels    5;  Gaps    2;
```

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S20066
pancreatic-type ribonuclease (EC 3.1.27.5) BRb precursor, brain - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 22-Nov-1993 #sequence_revision 12-May-1995 #text_change 22-Jun-1999
C;Accession: S20066; JX0056
R;Sasso, M.P.; Carsana, A.; Confalone, E.; Cosi, C.; Sorrentino, S.; Viola, M.; Palmieri
Nucleic Acids Res. 19, 6469-6474, 1991
A;Title: Molecular cloning of the gene encoding the bovine brain ribonuclease and its ex
A;Reference number: S20066; MUID:92093604; PMID:1754384
A;Accession: S20066
A;Molecule type: DNA
A;Residues: 1-167 <SAS>
A;Cross-references: EMBL:X59767; NID:g150; PIDN:CAA42439.1; PID:g151
R;Watanabe, H.; Katoh, H.; Ishii, M.; Komoda, Y.; Sanda, A.; Takizawa, Y.; Ohgi, K.; Iri
J. Biochem. 104, 939-945, 1988
A;Title: Primary structure of a ribonuclease from bovine brain.
A;Reference number: JX0056; MUID:89214015; PMID:3243767
A;Accession: JX0056
A;Molecule type: protein
A;Residues: 27-154,'S',156-166 <WAT>
A;Experimental source: brain
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase
F;38,67,145/Active site: His, Lys, His #status predicted
F;52-110,66-121,84-136,91-98/Disulfide bonds: #status predicted
F;88/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;155/Binding site: carbohydrate (Thr) (covalent) #status experimental
F;159/Binding site: carbohydrate (Ser) (covalent) #status experimental

  Query Match             22.2%;  Score 133.5;  DB 2;  Length 167;
  Best Local Similarity   31.4%;  Pred. No. 3.6e-06;
  Matches   38;  Conservative   17;  Mismatches   43;  Indels   23;  Gaps    7;

Qy          4 ATFQQKHI------INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINM 57
              | |:::|:       : |  || :|     :  |:|| ||||:  |   |||:|:
Db         32 AKFRRQHMDSGSSSSSNPNYCNQMMKRR-RMTHGRCKPVNTFVHESLDDVKAVCS---QK 87

Qy         58 NVL----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHFA 104
              |:          | :   :  |  |  :  | | | :   :   || | || | | ||||
Db         88 NITCKNGHPNCYQSKSTMSITDCRETGSSKYPNCAYKTSQKQKYITVACEGNPYVPVHFD 147

Qy        105 G 105
              |
Db        148 G 148


RESULT 8
NRPG
pancreatic ribonuclease (EC 3.1.27.5) - pig
N;Alternate names: RNase 1; RNase A
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
C;Accession: A92071; A91391; A00816
R;Jackson, R.L.; Hirs, C.H.W.
J. Biol. Chem. 245, 637-653, 1970
A;Title: The primary structure of porcine pancreatic ribonuclease. II. The amino acid se
A;Reference number: A92071; MUID:70104197; PMID:5460946
A;Accession: A92071
A;Molecule type: protein
A;Residues: 1,'Q',3-124 <JAC>
R;Wierenga, R.K.; Huizinga, J.D.; Gaastra, W.; Welling, G.W.; Beintema, J.J.
FEBS Lett. 31, 181-185, 1973
A;Title: Affinity chromatography of porcine pancreatic ribonuclease and reinvestigation
A;Reference number: A91391
A;Accession: A91391
A;Molecule type: protein
A;Residues: 1-124 <WIE>
R;Phelan, J.J.; Hirs, C.H.W.
J. Biol. Chem. 245, 654-661, 1970
A;Title: The primary structure of porcine pancreatic ribonuclease. III. The disulfide bo
A;Reference number: A92072; MUID:70104198; PMID:4904878
A;Contents: annotation; disulfide bonds
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;21,34,76/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status experimental

  Query Match             22.0%;  Score 132.5;  DB 1;  Length 124;
  Best Local Similarity   31.6%;  Pred. No. 3.4e-06;
  Matches   36;  Conservative   19;  Mismatches   42;  Indels   17;  Gaps    6;

Qy          6 FQQKHI------INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGV-INMN 58
              ||::|:       |:   || :|     :  |:|| ||||:  |   |:|:|: : :|
Db          8 FQRQHMDPDSSSSNSSNYCNLMMSRR-NMTQGRCKPVNTFVHESLADVQAVCSQINVNCK 66

Qy         59 VLSTTRFQLNT------CTRTSITPRP-CPYSSRTETNYICVKCENQ--YPVHF 103
                |  :| |:       | :|  :  | | | :  |  :| | ||     ||||
Db         67 NGQTNCYQSNSTMHITDCRQTGSSKYPNCAYKASQEQKHIIVACEGNPPVPVHF 120


RESULT 9
S41111
pancreatic ribonuclease - common iguana
C;Species: Iguana iguana (common iguana)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Aug-1998
C;Accession: S41111
R;Zhao, W.; Beintema, J.J.; Hofsteenge, J.
Eur. J. Biochem. 219, 641-646, 1994
A;Title: The amino acid sequence of iguana (Iguana iguana) pancreatic ribonuclease.
A;Reference number: S41111; MUID:94139745; PMID:8307028
A;Accession: S41111
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-119 <ZHA>
C;Superfamily: pancreatic ribonuclease

  Query Match             21.0%;  Score 126.5;  DB 2;  Length 119;
  Best Local Similarity   29.8%;  Pred. No. 1.3e-05;
  Matches   34;  Conservative   16;  Mismatches   51;  Indels   13;  Gaps    4;

Qy          2 NWATFQQKHI-------INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAIC--- 51
              :|::|| |||         |    |: :|     :   :||  |||: :| : :: :|
Db          2 DWSSFQNKHIDYPETSASNPNAYCDLMMQRR-NLNPTKCKTRNTFVHASPSEIQQVCGSG 60

Qy         52 -TGVINMNVLSTTRFQLNTCTRTSIT-PRPCPYSSRTETNYICVKCENQYPVHF 103
               |   :    |   | |  |     | |  | |:    |  | : |||  ||||
Db         61 GTHYEDNLYDSNESFDLTDCKNVGGTAPSSCKYNGTPGTKRIRIACENNQPVHF 114


RESULT 10
NRPRH
pancreatic ribonuclease (EC 3.1.27.5) - pronghorn (tentative sequence)
N;Alternate names: RNase 1; RNase A
C;Species: Antilocapra americana (pronghorn)
C;Date: 28-Feb-1981 #sequence_revision 28-Feb-1981 #text_change 31-Mar-2000
C;Accession: A00813
R;Beintema, J.J.; Gaastra, W.; Munniksma, J.
J. Mol. Evol. 13, 305-316, 1979
A;Title: Primary structure of pronghorn pancreatic ribonuclease: close relationship bet
A;Reference number: A00813; MUID:80075014; PMID:513141
A;Accession: A00813
A;Molecule type: protein
A;Residues: 1-124 <BEI>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F;34/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

  Query Match             20.4%;  Score 122.5;  DB 1;  Length 124;
  Best Local Similarity   30.3%;  Pred. No. 3.3e-05;
  Matches   36;  Conservative   18;  Mismatches   42;  Indels   23;  Gaps    7;

Qy          4 ATFQQKHIINTPI------ICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINM 57
              | |:::|| : |        || :| :   :  |:|| ||||:  |   |:|:|:
```

```
Qy          2 NWATFQQKHIINTP-IICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGV-INMNV 59
              ||| ||:||| ||  | |||||| :|||||||||  ||||||||||||||:|   | ||
Db          2 NWAKFQEKHIPNTSNINCNTIMDKSIYIVGGQCKERNTFIISSATTVKAICSGASTNRNV 61

Qy         60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              |||||||||| |::  |||||:|||||| |||||||: ||||||||||
Db         62 LSTTRFQLNTCIRSATAPRPCPYNSRTETNVICVKCENRLPVHFAGIGRC 111


RESULT 3
JX0085
pancreatic ribonuclease (EC 3.1.27.5) - bullfrog
C;Species: Rana catesbeiana (bullfrog)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994
C;Accession: JX0085
R;Nitta, R.; Katayama, N.; Okabe, Y.; Iwama, M.; Watanabe, H.; Abe, Y.; Okazaki, T.; Ohg
J. Biochem. 106, 729-735, 1989
A;Title: Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver.
A;Reference number: JX0085; MUID:90130374; PMID:2613682
A;Accession: JX0085
A;Molecule type: protein
A;Residues: 1-111 <NIT>
C;Superfamily: pancreatic ribonuclease
C;Keywords: hydrolase; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10,35,104/Active site: His, Lys, His #status predicted
F;19-72,34-82,52-97,94-111/Disulfide bonds: #status predicted

  Query Match             61.4%;  Score 369;  DB 2;  Length 111;
  Best Local Similarity   65.5%;  Pred. No. 9.6e-30;
  Matches   72;  Conservative    9;  Mismatches   27;  Indels    2;  Gaps    2;

Qy          2 NWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMNV 59
              ||| |::||| :|  | |||||| ||||||:||  |||||||   |||||:||  :
Db          2 NWAKFKEKHIRSTSSIDCNTIMDKAIYIVGGKCKERNTFIISSEDNVKAICSGVSPDRKE 61

Qy         60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              |||| |:|||| | |||||||||    : | |||||| | |||| |||:|
Db         62 LSTTSFKLNTCIRDSITPRPCPYHPSPDNNKICVKCEKQLPVHFVGIGKC 111


RESULT 4
A39035
ribonuclease-related anti-tumor protein - northern leopard frog (fragment)
C;Species: Rana pipiens (northern leopard frog)
C;Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993
C;Accession: A39035
R;Ardelt, W.; Mikulski, S.M.; Shogen, K.
J. Biol. Chem. 266, 245-251, 1991
A;Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and earl
A;Reference number: A39035; MUID:91093131; PMID:1985896
A;Accession: A39035
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-104 <ARD>
C;Superfamily: pancreatic ribonuclease

  Query Match             45.3%;  Score 272.5;  DB 2;  Length 104;
  Best Local Similarity   49.1%;  Pred. No. 3.5e-20;
  Matches   54;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          2 NWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMNV 59
              :| |||:||| ||  : |: ||  |::     ||  |||| |    ||||| |:| : ||
Db          2 DWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV 57

Qy         60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              |:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         58 LTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104


RESULT 5
NRWHK
pancreatic ribonuclease (EC 3.1.27.5) - minke whale
N;Alternate names: RNase 1; RNase A
C;Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
C;Accession: A00818
R;Emmens, M.; Welling, G.W.; Beintema, J.J.
Biochem. J. 157, 317-323, 1976
A;Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclease.
A;Reference number: A00818; MUID:76277855; PMID:962870
A;Accession: A00818
A;Molecule type: protein
A;Residues: 1-124 <EMM>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F;76/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

  Query Match             22.5%;  Score 135.5;  DB 1;  Length 124;
  Best Local Similarity   33.3%;  Pred. No. 1.7e-06;
  Matches   39;  Conservative   16;  Mismatches   39;  Indels   23;  Gaps    7;

Qy          6 FQQKHII------NTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 59
              ||::|:       | |  || :|     :  |:|| ||||:  |   |||:|:     ||
Db          8 FQRQHMDSGNSPGNNPNYCNQMMMRR-KMTQGRCKPVNTFVHESLEDVKAVCS---QKNV 63

Qy         60 L----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 103
              |          | :   :  | :|  :  | | | :   :  :| | || | | ||||
Db         64 LCKNGRTNCYESNSTMHITDCRQTGSSKYPNCAYKTSQKEKHIIVACEGNPYVPVHF 120


RESULT 6
A35932
angiogenin precursor - mouse
N;Alternate names: angiogenesis factor
N;Contains: ribonuclease (EC 3.1.27.-)
C;Species: Mus musculus (house mouse)
C;Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 18-Jun-1999
C;Accession: A35932
R;Bond, M.D.; Vallee, B.L.
Biochem. Biophys. Res. Commun. 171, 988-995, 1990
A;Title: Isolation and sequencing of mouse angiogenin DNA.
A;Reference number: A35932; MUID:91025023; PMID:2222458
A;Accession: A35932
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-145 <BON>
A;Cross-references: GB:U22516; NID:g726325; PIDN:AAA91366.1; PID:g726326
C;Genetics:
A;Introns: #status absent
C;Function:
A;Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues
C;Superfamily: pancreatic ribonuclease
C;Keywords: angiogenesis; hydrolase; nucleic acid degradation; pyroglutamic acid
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-145/Product: angiogenin #status predicted <MAT>
F;25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;37,64,137/Active site: His, Lys, His #status predicted
F;50-104,63-115,81-130/Disulfide bonds: #status predicted

  Query Match             22.5%;  Score 135.5;  DB 1;  Length 145;
  Best Local Similarity   39.5%;  Pred. No. 2e-06;
  Matches   30;  Conservative   12;  Mismatches   29;  Indels    5;  Gaps    3;

Qy         33 CKRVNTFIISSATTVKAIC---TGVINMNV-LSTTRFQLNTCTRTSITPR-PCPYSSRTE 87
              || |||||  : : :||||         |: :| : ||: ||  |  :|| || | :
Db         63 CKDVNTFIHGNKSNIKAICGANGSPYRENLRMSKSPFQVTTCKHTGGSPRPPCQYRASAG 122

Qy         88 TNYICVKCENQYPVHF 103
                :: : |||  ||||
Db        123 FRHVVIACENGLPVHF 138


RESULT 7
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 11, 2004, 14:31:13 ; Search time 13.4389 Seconds
(without alignments)
787.345 Million cell updates/sec

Title: US-09-961-400-24
Perfect score: 601
Sequence: 1 SNWATFQQKHIINTPIICNT.....ICVKCENQYPVHFAGIGRCP 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	586.5	97.6	111	2	A27121	ribonuclease-relat
2	450	74.9	111	1	JX0120	ribonuclease-relat
3	369	61.4	111	2	JX0085	pancreatic ribonuc
4	272.5	45.3	104	2	A39035	ribonuclease-relat
5	135.5	22.5	124	1	NRWHK	pancreatic ribonuc
6	135.5	22.5	145	1	A35932	angiogenin precurs
7	133.5	22.2	167	2	S20066	pancreatic-type ri
8	132.5	22.0	124	1	NRPG	pancreatic ribonuc
9	126.5	21.0	119	2	S41111	pancreatic ribonuc
10	122.5	20.4	124	1	NRPRH	pancreatic ribonuc
11	122	20.3	122	1	NRKGR	pancreatic ribonuc
12	120.5	20.0	128	1	NRCU	pancreatic ribonuc
13	120.5	20.0	149	1	NRMS	pancreatic ribonuc
14	119.5	19.9	123	1	A43825	angiogenin - pig
15	118.5	19.7	128	1	NRGPB	pancreatic ribonuc
16	117.5	19.6	128	1	NRHO	pancreatic ribonuc
17	116.5	19.4	124	1	NRCM	pancreatic ribonuc
18	116.5	19.4	124	1	NRCMM	pancreatic ribonuc
19	116.5	19.4	124	1	NRCMB	pancreatic ribonuc
20	116.5	19.4	128	1	NRKS	pancreatic ribonuc
21	114.5	19.1	124	2	S08549	ribonuclease - dom
22	114	19.0	125	1	A32474	angiogenin [valida
23	113.5	18.9	124	1	NRDEN	pancreatic ribonuc
24	113.5	18.9	125	1	B43825	angiogenin - rabbi
25	113	18.8	147	1	NRHUAG	angiogenin precurs
26	112.5	18.7	124	1	NRGF	pancreatic ribonuc
27	112.5	18.7	124	1	NRDEO	pancreatic ribonuc
28	111.5	18.6	130	2	S22808	pancreatic ribonuc
29	110.5	18.4	124	1	NRBOB	pancreatic ribonuc
30	110.5	18.4	124	1	NRWB	pancreatic ribonuc
31	110.5	18.4	124	1	NREKN	pancreatic ribonuc
32	110.5	18.4	124	2	S07141	pancreatic ribonuc
33	110.5	18.4	150	1	NRBO	pancreatic ribonuc
34	110.5	18.4	158	2	I61900	eosinophil-derived
35	109.5	18.2	124	1	NRSH	pancreatic ribonuc
36	108.5	18.1	119	2	JX0115	pancreatic ribonuc
37	108.5	18.1	124	1	NRCB	pancreatic ribonuc
38	108.5	18.1	152	1	NRRT	pancreatic ribonuc
39	106.5	17.7	124	1	NRHP	pancreatic ribonuc
40	106.5	17.7	125	4	A47498	seminal ribonuclea
41	106.5	17.7	150	1	NRBOS	seminal ribonuclea
42	104.5	17.4	124	1	NRGN	pancreatic ribonuc
43	104.5	17.4	124	1	NRDEF	pancreatic ribonuc
44	104	17.3	125	2	S04503	pancreatic ribonuc
45	103.5	17.2	124	2	S08546	pancreatic ribonuc

ALIGNMENTS

RESULT 1
A27121
ribonuclease-related sialic acid-binding lectin - bullfrog
C;Species: Rana catesbeiana (bullfrog)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 30-Jun-1993
C;Accession: A27121
R;Titani, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kawauchi, H.; Takayanagi
Biochemistry 26, 2189-2194, 1987
A;Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana)
A;Reference number: A27121; MUID:87299649; PMID:3304421
A;Accession: A27121
A;Molecule type: protein
A;Residues: 1-111 <TIT>
C;Superfamily: pancreatic ribonuclease
C;Keywords: lectin

Query Match 97.6%; Score 586.5; DB 2; Length 111;
Best Local Similarity 99.1%; Pred. No. 2.3e-51;
Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```
Qy          2 NWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 60
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db          2 NWATFQQKHIINTPIINCNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 61

Qy         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
```

RESULT 2
JX0120
ribonuclease-related sialic acid-binding lectin - Japanese frog
C;Species: Rana japonica (Japanese frog)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JX0120
R;Kamiya, Y.; Oyama, F.; Oyama, R.; Sakakibara, F.; Nitta, K.; Kawauchi, H.; Takayanagi
J. Biochem. 108, 139-143, 1990
A;Title: Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs.
A;Reference number: JX0120; MUID:91035319; PMID:2229005
A;Accession: JX0120
A;Molecule type: protein
A;Residues: 1-111 <KAM>
A;Experimental source: egg
C;Superfamily: pancreatic ribonuclease
C;Keywords: lectin; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;19-72,34-82,52-97,94-111/Disulfide bonds: #status experimental

Query Match 74.9%; Score 450; DB 1; Length 111;
Best Local Similarity 78.2%; Pred. No. 8.6e-38;
Matches 86; Conservative 7; Mismatches 15; Indels 2; Gaps 2;

XX
PD 07-OCT-1999.
XX
PF 26-MAR-1999; 99WO-US006641.
XX
PR 27-MAR-1998; 98US-0079751P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rybak SM, Newton DL;
XX
DR WPI; 1999-610847/52.
DR N-PSDB; AAZ08136.
XX
PT New recombinant ribonucleases, used for killing target cells, e.g. for
PT treating cancers, viral infections or autoimmune diseases.
XX
PS Disclosure; Page 69; 71pp; English.
XX
CC The present sequence is a Rana pipiens Clone 5a1b ribonuclease (RaPLR1).
CC It is encoded by Clone 5a1b cDNA obtained from Rana pipiens liver mRNA
CC library. It exhibits differences with Onconase (RTM) at amino acid
CC residues 11, 20, 85 and 103. Carboxy terminal end of RaPLR1 has a
CC covalently bound ligand binding moiety, which can be a LL2 antibody
CC directed against CD22 on cancerous B cells or human chorionic
CC gonadotrophin (hCG) effective against Kaposi's Sarcoma cells. Recombinant
CC ribonucleases can be expressed in bacteria without an N-terminal
CC methionine due to the presence of a signal peptide that is cleaved by
CC bacteria. The soluble expression of ribonuclease allows the proteins to
CC be fused in-frame with ligand binding moieties to form cytotoxic fusion
CC proteins. They can be used for treatment of cancer and autoimmune
CC diseases
XX
SQ Sequence 127 AA;

Query Match 46.0%; Score 276.5; DB 2; Length 127;
Best Local Similarity 49.1%; Pred. No. 1.4e-23;
Matches 54; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

```
Qy          2 NWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMNV 59
              :| |||:||: ||  : || ||  |::     ||  |||| |    ||||| |:| : ||
Db         25 DWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV 80

Qy         60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                |:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         81 LTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 127
```

RESULT 15
AAW35134
ID AAW35134 standard; protein; 251 AA.
XX
AC AAW35134;
XX
DT 20-APR-1998 (first entry)
XX
DE R. pipiens recombinant RNase rOnc fusion protein 10.
XX
KW RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion;
KW tumour cell growth; frog.
XX
OS Rana pipiens.
OS Synthetic.
XX
PN WO9731116-A2.
XX
PD 28-AUG-1997.
XX
PF 19-FEB-1997; 97WO-US002588.
XX
PR 21-FEB-1996; 96US-0011800P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rybak SM, Newton DL, Boque L, Wlodawer A;
XX
DR WPI; 1997-435168/40.
DR N-PSDB; AAT94972.
XX
PT Ribonuclease molecules based on native Onconase - used for killing cells,
PT particularly tumour cells.
XX
PS Disclosure; Page 76; 90pp; English.
XX
CC Sequences AAW35125 to AAW35135 represent recombinant fusion proteins
CC (rOnc) which are modifications of the RNase Onconase (RTM) (nOnc). Such
CC novel ribonuclease molecules are highly cytotoxic and can be used alone
CC or to form chemical conjugates or to target recombinant immunofusions.
CC They are used particularly for decreasing tumour cell growth. They can
CC also be used for cell separation in vitro by selectively killing unwanted
CC types of cells, e.g. in bone marrow prior to transplantation into a
CC patient undergoing marrow ablation by radiation, or for killing leukaemia
CC cells or T-cells that would cause graft versus host disease. The toxins
CC can also be used to selectively kill unwanted cells in culture. The new
CC ribonucleases have increased cytotoxic activity compared to nOnc and also
CC lower immunogenicity in humans
XX
SQ Sequence 251 AA;

Query Match 46.0%; Score 276.5; DB 2; Length 251;
Best Local Similarity 49.5%; Pred. No. 3.3e-23;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

```
Qy          1 SNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 58
              |:| |||:||| ||  : |: ||  |::     ||  |||| |    ||||| |:| : |
Db        148 SDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 203

Qy         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db        204 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 251
```

Search completed: May 11, 2004, 14:34:32
Job time : 51.2715 secs

```
KW   recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
KW   autoimmune disease.
XX
OS   Rana pipiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
FT                   /note= "Met not found in wild type RaPLR1"
XX
PN   WO9950398-A2.
XX
PD   07-OCT-1999.
XX
PF   26-MAR-1999;   99WO-US006641.
XX
PR   27-MAR-1998;   98US-0079751P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL;
XX
DR   WPI; 1999-610847/52.
DR   N-PSDB; AAZ08126.
XX
PT   New recombinant ribonucleases, used for killing target cells, e.g. for
PT   treating cancers, viral infections or autoimmune diseases.
XX
PS   Claim 34; Page 57; 71pp; English.
XX
CC   The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1)
CC   protein with Met at position 1. Carboxy terminal end of recombinant
CC   RaPLR1 has a covalently bound ligand binding moiety, which can be a LL2
CC   antibody directed against CD22 on cancerous B cells or human chorionic
CC   gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant
CC   ribonucleases can be expressed in bacteria without an N-terminal
CC   methionine due to the presence of a signal peptide that is cleaved by
CC   bacteria. The soluble expression of ribonuclease allows the proteins to
CC   be fused in-frame with ligand binding moieties to form cytotoxic fusion
CC   proteins. They can be used for treatment of cancer and autoimmune
CC   diseases
XX
SQ   Sequence 105 AA;

  Query Match             46.0%;  Score 276.5;  DB 2;  Length 105;
  Best Local Similarity   49.1%;  Pred. No. 1.1e-23;
  Matches   54;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          2 NWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMNV 59
              :| |||:||: ||  : || ||  |::     ||  |||| |    ||||| |:| : ||
Db          3 DWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV 58

Qy         60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              |:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         59 LTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105


RESULT 13
AAW35118
ID   AAW35118 standard; protein; 112 AA.
XX
AC   AAW35118;
XX
DT   20-APR-1998  (first entry)
XX
DE   R. pipiens recombinant RNase protein NLSMetSerrOnc.
XX
KW   RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion;
KW   tumour cell growth; frog.
XX
OS   Rana pipiens.
XX
PN   WO9731116-A2.
XX
PD   28-AUG-1997.
XX
PF   19-FEB-1997;   97WO-US002588.
XX
PR   21-FEB-1996;   96US-0011800P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL,  Boque L,  Wlodawer A;
XX
DR   WPI; 1997-435168/40.
DR   N-PSDB; AAT94955.
XX
PT   Ribonuclease molecules based on native Onconase - used for killing cells,
PT   particularly tumour cells.
XX
PS   Claim 18; Page 63; 90pp; English.
XX
CC   AAW35115 to AAW35123 encode recombinant proteins (rOnc) which are
CC   modifications of the RNase Onconase (RTM) (nOnc). Such novel ribonuclease
CC   molecules are highly cytotoxic and can be used alone or to form chemical
CC   conjugates or to target recombinant immunofusions. They are used
CC   particularly for decreasing tumour cell growth. They can also be used for
CC   cell separation in vitro by selectively killing unwanted types of cells,
CC   e.g. in bone marrow prior to transplantation into a patient undergoing
CC   marrow ablation by radiation, or for killing leukaemia cells or T-cells
CC   that would cause graft versus host disease. The toxins can also be used
CC   to selectively kill unwanted cells in culture. The new ribonucleases have
CC   increased cytotoxic activity compared to nOnc and also lower
CC   immunogenicity in humans
XX
SQ   Sequence 112 AA;

  Query Match             46.0%;  Score 276.5;  DB 2;  Length 112;
  Best Local Similarity   49.5%;  Pred. No. 1.2e-23;
  Matches   55;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          1 SNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 58
              |:| |||:||| ||  : |: ||  |::     ||  |||| |    ||||| |:| : |
Db          9 SDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 64

Qy         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         65 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 112


RESULT 14
AAY28879
ID   AAY28879 standard; protein; 127 AA.
XX
AC   AAY28879;
XX
DT   25-JAN-2000  (first entry)
XX
DE   Rana pipiens Clone 5a1b ribonuclease.
XX
KW   Rana pipiens ribonuclease Clone 5a1b; RaPLR1; covalently bound; RNase;
KW   LL2 antibody; ligand binding moiety; CD22; cancerous B cell; onconase;
KW   Kaposi's Sarcoma; human chorionic gonadotrophin; hCG; cancer;
KW   recombinant ribonuclease; frog; signal peptide; cytotoxic fusion protein;
KW   autoimmune disease.
XX
OS   Rana pipiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /label= Signal_peptide
FT                   /note= "Putative"
FT   Protein         24. .127
FT                   /label= Rana_pipiens_Clone_5a1b_ribonuclease
XX
PN   WO9950398-A2.
```

```
ID   AAY28871 standard; protein; 105 AA.
XX
AC   AAY28871;
XX
DT   25-JAN-2000  (first entry)
XX
DE   Recombinant Met(-1) RaPLR1 Gln1Ser amino acid sequence.
XX
KW   Recombinant Met(-1) Rana pipiens ribonuclease Gln1Ser; RaPLR1; CD22;
KW   covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
KW   Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
KW   recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
KW   autoimmune disease; RNase.
XX
OS   Rana pipiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
FT                   /note= "Met not found in wild type RaPLR1"
FT   Misc-difference 2
FT                   /note= "Wild type Gln replaced with Ser"
XX
PN   WO9950398-A2.
XX
PD   07-OCT-1999.
XX
PF   26-MAR-1999;   99WO-US006641.
XX
PR   27-MAR-1998;   98US-0079751P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL;
XX
DR   WPI; 1999-610847/52.
DR   N-PSDB; AAZ08129.
XX
PT   New recombinant ribonucleases, used for killing target cells, e.g. for
PT   treating cancers, viral infections or autoimmune diseases.
XX
PS   Claim 34; Page 61; 71pp; English.
XX
CC   The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1)
CC   protein with Met at position 1 and Gln2Ser. Carboxy terminal end of
CC   recombinant RaPLR1 has a covalently bound ligand binding moiety, which
CC   can be a LL2 antibody directed against CD22 on cancerous B cells or human
CC   chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells.
CC   Recombinant ribonucleases can be expressed in bacteria without an N-
CC   terminal methionine due to the presence of a signal peptide that is
CC   cleaved by bacteria. The soluble expression of ribonuclease allows the
CC   proteins to be fused in-frame with ligand binding moieties to form
CC   cytotoxic fusion proteins. They can be used for treatment of cancer and
CC   autoimmune diseases
XX
SQ   Sequence 105 AA;

  Query Match             46.7%;  Score 280.5;  DB 2;  Length 105;
  Best Local Similarity   49.5%;  Pred. No. 3.9e-24;
  Matches   55;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          1 SNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 58
              |:| |||:||: ||  : || ||  |::     ||  |||| |    ||||| |:| : |
Db          2 SDWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 57

Qy         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         58 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105


RESULT 11
AAY28865
ID   AAY28865 standard; protein; 104 AA.
XX
AC   AAY28865;
XX
DT   25-JAN-2000  (first entry)
XX
DE   Rana pipiens liver ribonuclease (RaPLR1).
XX
KW   Rana pipiens liver ribonuclease; RaPLR1; covalently bound; LL2 antibody;
KW   ligand binding moiety; CD22; cancerous B cell; Kaposi's Sarcoma; frog;
KW   human chorionic gonadotrophin; hCG; recombinant ribonuclease; RNase;
KW   signal peptide; cytotoxic fusion protein; cancer; autoimmune disease.
XX
OS   Rana pipiens.
XX
PN   WO9950398-A2.
XX
PD   07-OCT-1999.
XX
PF   26-MAR-1999;   99WO-US006641.
XX
PR   27-MAR-1998;   98US-0079751P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL;
XX
DR   WPI; 1999-610847/52.
DR   N-PSDB; AAZ08124.
XX
PT   New recombinant ribonucleases, used for killing target cells, e.g. for
PT   treating cancers, viral infections or autoimmune diseases.
XX
PS   Claim 1; Page 55; 71pp; English.
XX
CC   The present sequence is Rana pipiens liver ribonuclease (RaPLR1) protein.
CC   Carboxy terminal end of RaPLR1 has a covalently bound ligand binding
CC   moiety, which can be a LL2 antibody directed against CD22 on cancerous B
CC   cells or human chorionic gonadotrophin (hCG) effective against Kaposi's
CC   Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria
CC   without an N-terminal methionine due to the presence of a signal peptide
CC   that is cleaved by bacteria. The soluble expression of ribonuclease
CC   allows the proteins to be fused in-frame with ligand binding moieties to
CC   form cytotoxic fusion proteins. They can be used for treatment of cancer
CC   and autoimmune diseases
XX
SQ   Sequence 104 AA;

  Query Match             46.0%;  Score 276.5;  DB 2;  Length 104;
  Best Local Similarity   49.1%;  Pred. No. 1.1e-23;
  Matches   54;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          2 NWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMNV 59
              :| |||:||: ||  : || ||  |::     ||  |||| |    ||||| |:| : ||
Db          2 DWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV 57

Qy         60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              |:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         58 LTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104


RESULT 12
AAY28867
ID   AAY28867 standard; protein; 105 AA.
XX
AC   AAY28867;
XX
DT   25-JAN-2000  (first entry)
XX
DE   Recombinant Met(-1) RaPLR1.
XX
KW   Recombinant Met(-1) Rana pipiens ribonuclease; RaPLR1; CD22; RNase;
KW   covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
KW   Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
```

```
CC   (Rana catesbeiana) lectin used to describe the method of the invention
XX
SQ   Sequence 111 AA;

  Query Match             97.6%;  Score 586.5;  DB 2;  Length 111;
  Best Local Similarity   99.1%;  Pred. No. 3.8e-59;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          2 NWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 60
              |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db          2 NWATFQQKHIINTPIINCNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 61

Qy         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111


RESULT 8
AAW06544
ID   AAW06544 standard; protein; 104 AA.
XX
AC   AAW06544;
XX
DT   22-AUG-1997  (first entry)
XX
DE   Antitumour protein from Rana pipiens oocytes.
XX
KW   Tumour; chemotherapy; radiotherapy; frog.
XX
OS   Rana pipiens.
XX
PN   WO9639428-A1.
XX
PD   12-DEC-1996.
XX
PF   03-JUN-1996;   96WO-US008304.
XX
PR   06-JUN-1995;   95US-00467955.
XX
PA   (ALFA-) ALFACELL CORP.
XX
PI   Ardelt WJ;
XX
DR   WPI; 1997-043063/04.
XX
PT   Antitumour proteins from Rana pipiens oocyte(s) - have fewer
PT   disadvantages than chemotherapy, surgery and radiotherapy.
XX
PS   Claim 8; Page 28; 45pp; English.
XX
CC   The present sequence is a specifically claimed example of an antitumour
CC   protein from the generic protein in AAW18224, with the molecular weight
CC   12000. This is one of two preferred proteins (the other in AAW06543) that
CC   have been isolated from Rana pipiens oocytes. Both proteins have a
CC   blocked amino terminal group and are essentially free of carbohydrates.
CC   The proteins are used to treat tumours. Use of the peptides has fewer
CC   disadvantages than chemotherapy, radiotherapy and surgery in the
CC   treatment of tumours
XX
SQ   Sequence 104 AA;

  Query Match             47.0%;  Score 282.5;  DB 2;  Length 104;
  Best Local Similarity   50.0%;  Pred. No. 2.3e-24;
  Matches   55;  Conservative   15;  Mismatches   31;  Indels    9;  Gaps    4;

Qy          2 NWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMNV 59
              :| |||:||: ||  : || ||  |::     ||  |||| |    ||||| |:| : ||
Db          2 DWLTFQKKHVTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV 57

Qy         60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              |:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:|||
Db         58 LTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGRC 104


RESULT 9
AAY28870
ID   AAY28870 standard; protein; 104 AA.
XX
AC   AAY28870;
XX
DT   25-JAN-2000  (first entry)
XX
DE   Recombinant RaPLR1 Gln1Ser amino acid sequence.
XX
KW   Recombinant Rana pipiens ribonuclease; RaPLR1 Gln1Ser; covalently bound;
KW   LL2 antibody; ligand binding moiety; CD22; cancerous B cell; frog;
KW   Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
KW   recombinant ribonuclease; cytotoxic fusion protein; cancer; RNase;
KW   autoimmune disease.
XX
OS   Rana pipiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
FT                   /note= "Wild type Gln replaced with Ser"
XX
PN   WO9950398-A2.
XX
PD   07-OCT-1999.
XX
PF   26-MAR-1999;   99WO-US006641.
XX
PR   27-MAR-1998;   98US-0079751P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL;
XX
DR   WPI; 1999-610847/52.
DR   N-PSDB; AAZ08128.
XX
PT   New recombinant ribonucleases, used for killing target cells, e.g. for
PT   treating cancers, viral infections or autoimmune diseases.
XX
PS   Claim 34; Page 60; 71pp; English.
XX
CC   The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1)
CC   protein with Gln1Ser. Carboxy terminal end of recombinant RaPLR1 has a
CC   covalently bound ligand binding moiety, which can be a LL2 antibody
CC   directed against CD22 on cancerous B cells or human chorionic
CC   gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant
CC   ribonucleases can be expressed in bacteria without an N-terminal
CC   methionine due to the presence of a signal peptide that is cleaved by
CC   bacteria. The soluble expression of ribonuclease allows the proteins to
CC   be fused in-frame with ligand binding moieties to form cytotoxic fusion
CC   proteins. They can be used for treatment of cancer and autoimmune
CC   diseases
XX
SQ   Sequence 104 AA;

  Query Match             46.7%;  Score 280.5;  DB 2;  Length 104;
  Best Local Similarity   49.5%;  Pred. No. 3.8e-24;
  Matches   55;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          1 SNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 58
              |:| |||:||: ||  : || ||  |::     ||  |||| |    ||||| |:| : |
Db          1 SDWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56

Qy         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104


RESULT 10
AAY28871
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Qy          2 NWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS 61
              ||||||||||||||||||:||||||||||||||||||||||||||||||:||||
Db          2 NWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVLS 61

Qy         62 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110


RESULT 6
AAY28876
ID   AAY28876 standard; protein; 111 AA.
XX
AC   AAY28876;
XX
DT   25-JAN-2000  (first entry)
XX
DE   Recombinant Met(-1) RaCOR1 Met22Leu Met57Leu-(His)6 protein.
XX
KW   Met(-1) Rana catesbeiana ribonuclease Met22Leu Met57Leu-(His)6; RaCOR1;
KW   recombinant; CD22; covalently bound; LL2 antibody; ligand binding moiety;
KW   cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG;
KW   signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
KW   cancer; bullfrog; RNase; autoimmune disease.
XX
OS   Rana catesbeiana.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
FT                   /note= "Met not found in wild type RaCOR1"
FT   Misc-difference 1
FT                   /note= "(His)6 histidine tag attached to N-terminal Met"
FT   Misc-difference 23
FT                   /note= "Wild type Met replaced with Leu"
FT   Misc-difference 58
FT                   /note= "Wild type Met replaced with Leu"
XX
PN   WO9950398-A2.
XX
PD   07-OCT-1999.
XX
PF   26-MAR-1999;   99WO-US006641.
XX
PR   27-MAR-1998;   98US-0079751P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL;
XX
DR   WPI; 1999-610847/52.
DR   N-PSDB; AAZ08133.
XX
PT   New recombinant ribonucleases, used for killing target cells, e.g. for
PT   treating cancers, viral infections or autoimmune diseases.
XX
PS   Claim 22; Page 66; 71pp; English.
XX
CC   The present sequence is a recombinant Rana catesbeiana oocyte
CC   ribonuclease (RaCOR1) protein with Met at position 1 attached to a (His)6
CC   tag, Met23Leu and Met58Leu. Carboxy terminal end of recombinant RaCOR1
CC   has a covalently bound ligand binding moiety, which can be a LL2 antibody
CC   directed against CD22 on cancerous B cells or human chorionic
CC   gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant
CC   ribonucleases can be expressed in bacteria without an N-terminal
CC   methionine due to the presence of a signal peptide that is cleaved by
CC   bacteria. The soluble expression of ribonuclease allows the proteins to
CC   be fused in-frame with ligand binding moieties to form cytotoxic fusion
CC   proteins. They can be used for treatment of cancer and autoimmune
CC   diseases
XX
SQ   Sequence 111 AA;
```

```
  Query Match           98.3%;  Score 591;  DB 2;  Length 111;
  Best Local Similarity  98.2%;  Pred. No. 1.2e-59;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 NWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS 61
              ||||||||||||||||||:||||||||||||||||||||||||||||||:||||
Db          3 NWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVLS 62

Qy         62 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111


RESULT 7
AAY33321
ID   AAY33321 standard; protein; 111 AA.
XX
AC   AAY33321;
XX
DT   29-NOV-1999  (first entry)
XX
DE   Frog lectin protein fragment.
XX
KW   Cytotoxic; RNase; ribonuclease; pancreatic; antibody; light chain;
KW   heavy chain; cell surface marker; treatment; tumor; viral infection;
KW   parasite infection; immune dysfunctional cell; autoimmune disease;
KW   contraceptive; cell separation; transplantation; bone marrow ablation;
KW   leukemia cell; T-cell; graft-versus-host disease; bullfrog; lectin.
XX
OS   Rana catesbeiana.
XX
PN   US5955073-A.
XX
PD   21-SEP-1999.
XX
PF   09-JUL-1997;   97US-00891848.
XX
PR   20-APR-1990;   90US-00510696.
PR   22-OCT-1991;   91US-00779195.
PR   04-FEB-1993;   93US-00014082.
PR   22-SEP-1993;   93US-00125462.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL,  Nicholls PJ,  Youle RJ;
XX
DR   WPI; 1999-560488/47.
XX
PT   Recombinantly fused pancreatic RNase-targeting proteins useful for
PT   treating tumors, infections, immune or autoimmune disorders and as a
PT   contraceptive.
XX
PS   Example 3; Fig 19; 47pp; English.
XX
CC   This invention describes a novel nucleic acid construct comprising
CC   sequences encoding functional pancreatic RNase and a second protein
CC   (preferably the light and heavy chains of an antibody) which binds a
CC   specific cell surface marker on a target cell and functions as a
CC   cytotoxic agent. The products can be used for selectively killing cells
CC   expressing a specific surface marker. They can be used for treating
CC   tumors or infected cells (e.g. cells infected by viruses (especially
CC   latent or chronic virus infections, such as human immunodeficiency virus
CC   (HIV)-1, Epstein-Barr virus, herpes viruses (herpes simplex types I and
CC   II), hepatitis viruses (B, non-A-non-B, and delta), herpes zoster,
CC   cytomegalovirus)) and cells infected with parasites (such as the malaria
CC   parasite)). They can also be used for treating immune dysfunctional cells
CC   in immune and autoimmune diseases. Additionally, they may be used as
CC   contraceptives. Finally they can also be used for cell separation in
CC   vitro by selectively killing unwanted types of cells (e.g. in bone
CC   marrow) prior to transplantation into a patient undergoing marrow
CC   ablation by radiation or for killing leukemia cells or T-cells that would
CC   cause graft-versus-host disease. This sequence represents a bullfrog
```

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  Query Match             99.3%;  Score 597;  DB 2;  Length 110;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-60;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 NWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 NWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS 61

Qy         62 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110


RESULT 4
AAY28873
ID   AAY28873 standard; protein; 111 AA.
XX
AC   AAY28873;
XX
DT   25-JAN-2000  (first entry)
XX
DE   Recombinant Met(-1) RaCOR1.
XX
KW   Recombinant Met(-1) Rana catesbeiana oocyte ribonuclease; RaCOR1; CD22;
KW   covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
KW   Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
KW   recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;
KW   RNase; autoimmune disease.
XX
OS   Rana catesbeiana.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
FT                   /note= "Met not found in wild type RaCOR1"
XX
PN   WO9950398-A2.
XX
PD   07-OCT-1999.
XX
PF   26-MAR-1999;   99WO-US006641.
XX
PR   27-MAR-1998;   98US-0079751P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL;
XX
DR   WPI; 1999-610847/52.
DR   N-PSDB; AAZ08131.
XX
PT   New recombinant ribonucleases, used for killing target cells, e.g. for
PT   treating cancers, viral infections or autoimmune diseases.
XX
PS   Claim 22; Page 63; 71pp; English.
XX
CC   The present sequence is a recombinant Rana catesbeiana oocyte
CC   ribonuclease (RaCOR1) protein with Met at position 1. Carboxy terminal
CC   end of recombinant RaCOR1 has a covalently bound ligand binding moiety,
CC   which can be a LL2 antibody directed against CD22 on cancerous B cells or
CC   human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma
CC   cells. Recombinant ribonucleases can be expressed in bacteria without an
CC   N-terminal methionine due to the presence of a signal peptide that is
CC   cleaved by bacteria. The soluble expression of ribonuclease allows the
CC   proteins to be fused in-frame with ligand binding moieties to form
CC   cytotoxic fusion proteins. They can be used for treatment of cancer and
CC   autoimmune diseases
XX
SQ   Sequence 111 AA;

  Query Match             99.3%;  Score 597;  DB 2;  Length 111;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-60;
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Qy          2 NWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 NWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS 62

Qy         62 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111


RESULT 5
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ID   AAY28874 standard; protein; 110 AA.
XX
AC   AAY28874;
XX
DT   25-JAN-2000  (first entry)
XX
DE   Recombinant RaCOR1 Met22Leu Met57Leu amino acid sequence.
XX
KW   Recombinant Rana catesbeiana oocyte ribonuclease; covalently bound;
KW   RaCOR1 Met22Leu Met57Leu; LL2 antibody; ligand binding moiety; CD22;
KW   cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG;
KW   signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
KW   cancer; bullfrog; RNase; autoimmune disease.
XX
OS   Rana catesbeiana.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 22
FT                   /note= "Wild type Met replaced with Leu"
FT   Misc-difference 57
FT                   /note= "Wild type Met replaced with Leu"
XX
PN   WO9950398-A2.
XX
PD   07-OCT-1999.
XX
PF   26-MAR-1999;   99WO-US006641.
XX
PR   27-MAR-1998;   98US-0079751P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL;
XX
DR   WPI; 1999-610847/52.
DR   N-PSDB; AAZ08132.
XX
PT   New recombinant ribonucleases, used for killing target cells, e.g. for
PT   treating cancers, viral infections or autoimmune diseases.
XX
PS   Claim 22; Page 64; 71pp; English.
XX
CC   The present sequence is a recombinant Rana catesbeiana oocyte
CC   ribonuclease (RaCOR1) protein with Met22Leu Met57Leu. Carboxy terminal
CC   end of recombinant RaCOR1 has a covalently bound ligand binding moiety,
CC   which can be a LL2 antibody directed against CD22 on cancerous B cells or
CC   human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma
CC   cells. Recombinant ribonucleases can be expressed in bacteria without an
CC   N-terminal methionine due to the presence of a signal peptide that is
CC   cleaved by bacteria. The soluble expression of ribonuclease allows the
CC   proteins to be fused in-frame with ligand binding moieties to form
CC   cytotoxic fusion proteins. They can be used for treatment of cancer and
CC   autoimmune diseases
XX
SQ   Sequence 110 AA;

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CC   Recombinant ribonucleases can be expressed in bacteria without an N-
CC   terminal methionine due to the presence of a signal peptide that is
CC   cleaved by bacteria. The soluble expression of ribonuclease allows the
CC   proteins to be fused in-frame with ligand binding moieties to form
CC   cytotoxic fusion proteins. They can be used for treatment of cancer and
CC   autoimmune diseases
XX
SQ   Sequence 110 AA;

  Query Match             100.0%;  Score 601;  DB 2;  Length 110;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-61;
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Qy          1 SNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 SNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 60

Qy         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110


RESULT 2
AAY28878
ID   AAY28878 standard; protein; 111 AA.
XX
AC   AAY28878;
XX
DT   25-JAN-2000  (first entry)
XX
DE   Recombinant Met(-1) RaCOR1 Gln1Ser amino acid sequence.
XX
KW   Recombinant Met(-1) Rana catesbeiana oocyte ribonuclease Gln1Ser; RaCOR1;
KW   covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
KW   Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
KW   recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;
KW   CD22; RNase; autoimmune disease.
XX
OS   Rana catesbeiana.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
FT                   /note= "Met not found in wild type RaCOR1"
FT   Misc-difference 2
FT                   /note= "Wild type Gln replaced with Ser"
XX
PN   WO9950398-A2.
XX
PD   07-OCT-1999.
XX
PF   26-MAR-1999;   99WO-US006641.
XX
PR   27-MAR-1998;   98US-0079751P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL;
XX
DR   WPI; 1999-610847/52.
DR   N-PSDB; AAZ08135.
XX
PT   New recombinant ribonucleases, used for killing target cells, e.g. for
PT   treating cancers, viral infections or autoimmune diseases.
XX
PS   Claim 22; Page 68; 71pp; English.
XX
CC   The present sequence is a recombinant Rana catesbeiana ribonuclease
CC   (RaCOR1) protein with Met at position 1 and Gln2Ser. Carboxy terminal end
CC   of recombinant RaCOR1 has a covalently bound ligand binding moiety, which
CC   can be a LL2 antibody directed against CD22 on cancerous B cells or human
CC   chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells.
CC   Recombinant ribonucleases can be expressed in bacteria without an N-
CC   terminal methionine due to the presence of a signal peptide that is
CC   cleaved by bacteria. The soluble expression of ribonuclease allows the
CC   proteins to be fused in-frame with ligand binding moieties to form
CC   cytotoxic fusion proteins. They can be used for treatment of cancer and
CC   autoimmune diseases
XX
SQ   Sequence 111 AA;

  Query Match             100.0%;  Score 601;  DB 2;  Length 111;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-61;
  Matches  110;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 SNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 61

Qy         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111


RESULT 3
AAY28872
ID   AAY28872 standard; protein; 110 AA.
XX
AC   AAY28872;
XX
DT   25-JAN-2000  (first entry)
XX
DE   Rana catesbeiana oocyte ribonuclease (RaCOR1) amino acid sequence.
XX
KW   Rana catesbeiana oocyte ribonuclease; RaCOR1; covalently bound; CD22;
KW   LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's Sarcoma;
KW   human chorionic gonadotrophin; hCG; recombinant ribonuclease; bullfrog;
KW   signal peptide; cytotoxic fusion protein; cancer; autoimmune disease;
KW   RNase.
XX
OS   Rana catesbeiana.
OS   Synthetic.
XX
PN   WO9950398-A2.
XX
PD   07-OCT-1999.
XX
PF   26-MAR-1999;   99WO-US006641.
XX
PR   27-MAR-1998;   98US-0079751P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL;
XX
DR   WPI; 1999-610847/52.
DR   N-PSDB; AAZ08130.
XX
PT   New recombinant ribonucleases, used for killing target cells, e.g. for
PT   treating cancers, viral infections or autoimmune diseases.
XX
PS   Claim 22; Page 62; 71pp; English.
XX
CC   The present sequence is a Rana catesbeiana oocyte ribonuclease (RaCOR1)
CC   protein encoded by a cDNA modified for expression in E. coli. Carboxy
CC   terminal end of RaCOR1 has a covalently bound ligand binding moiety,
CC   which can be a LL2 antibody directed against CD22 on cancerous B cells or
CC   human chorionic gonadotrophin (hCG) effective against Kaposi's Sarcoma
CC   cells. Recombinant ribonucleases can be expressed in bacteria without an
CC   N-terminal methionine due to the presence of a signal peptide that is
CC   cleaved by bacteria. The soluble expression of ribonuclease allows the
CC   proteins to be fused in-frame with ligand binding moieties to form
CC   cytotoxic fusion proteins. They can be used for treatment of cancer and
CC   autoimmune diseases
XX
SQ   Sequence 110 AA;
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 11, 2004, 14:23:43 ; Search time 50.2715 Seconds
(without alignments)
618.248 Million cell updates/sec

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Perfect score: 601
Sequence: 1 SNWATFQQKHIINTPIICNT.....ICVKCENQYPVHFAGIGRCP 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	601	100.0	111	2	AAY28878	Aay28878 Recombina
3	597	99.3	110	2	AAY28872	Aay28872 Rana cate
4	597	99.3	111	2	AAY28873	Aay28873 Recombina
5	591	98.3	110	2	AAY28874	Aay28874 Recombina
6	591	98.3	111	2	AAY28876	Aay28876 Recombina
7	586.5	97.6	111	2	AAY33321	Aay33321 Frog lect
8	282.5	47.0	104	2	AAW06544	Aaw06544 Antitumou
9	280.5	46.7	104	2	AAY28870	Aay28870 Recombina
10	280.5	46.7	105	2	AAY28871	Aay28871 Recombina
11	276.5	46.0	104	2	AAY28865	Aay28865 Rana pipi
12	276.5	46.0	105	2	AAY28867	Aay28867 Recombina
13	276.5	46.0	112	2	AAW35118	Aaw35118 R. pipien
14	276.5	46.0	127	2	AAY28879	Aay28879 Rana pipi
15	276.5	46.0	251	2	AAW35134	Aaw35134 R. pipien
16	276.5	46.0	254	2	AAW35135	Aaw35135 R. pipien
17	276.5	46.0	355	2	AAW35133	Aaw35133 R. pipien
18	276.5	46.0	355	2	AAW35129	Aaw35129 R. pipien
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20	273.5	45.5	104	2	AAY28866	Aay28866 Recombina
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22	272.5	45.3	104	2	AAR12344	Aar12344 Protein w
23	272.5	45.3	104	2	AAR47303	Aar47303 ONCONASE
24	272.5	45.3	104	2	AAW00736	Aaw00736 Protein d
25	272.5	45.3	104	2	AAW14065	Aaw14065 Onconase
26	272.5	45.3	104	2	AAW06543	Aaw06543 Antitumou
27	272.5	45.3	104	2	AAW30301	Aaw30301 Recombina
28	272.5	45.3	104	2	AAW88233	Aaw88233 Rana pipi
29	272.5	45.3	104	2	AAY33322	Aay33322 Frog onco
30	272.5	45.3	104	4	AAB31666	Aab31666 Amino aci
31	272.5	45.3	104	5	ABG32650	Abg32650 Northern
32	272.5	45.3	105	2	AAW35123	Aaw35123 R. pipien
33	272.5	45.3	105	2	AAY39400	Aay39400 Recombina
34	272.5	45.3	106	2	AAW35122	Aaw35122 R. pipien
35	272.5	45.3	107	2	AAW35117	Aaw35117 R. pipien
36	272.5	45.3	355	2	AAW35125	Aaw35125 R. pipien
37	272.5	45.3	358	2	AAW35130	Aaw35130 R. pipien
38	272.5	45.3	379	2	AAW35126	Aaw35126 R. pipien
39	271.5	45.2	105	2	AAW35116	Aaw35116 R. pipien
40	269.5	44.8	104	2	AAW30302	Aaw30302 Recombina
41	267.5	44.5	104	4	AAB31667	Aab31667 Amino aci
42	267.5	44.5	104	5	ABG31617	Abg31617 Northern
43	267.5	44.5	105	2	AAW35115	Aaw35115 R. pipien
44	267.5	44.5	358	2	AAW35127	Aaw35127 R. pipien
45	267.5	44.5	365	2	AAW35131	Aaw35131 R. pipien

ALIGNMENTS

RESULT 1
AAY28877
ID AAY28877 standard; protein; 110 AA.
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AC AAY28877;
XX
DT 25-JAN-2000 (first entry)
XX
DE Recombinant RaCOR1 Gln1Ser amino acid sequence.
XX
KW Recombinant Rana catesbeiana oocyte ribonuclease; RaCOR1 Gln1Ser; CD22;
KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
KW bullfrog; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; RNase;
KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
KW cancer; autoimmune disease.
XX
OS Rana catesbeiana.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1
FT /note= "Wild type Gln replaced with Ser"
XX
PN WO9950398-A2.
XX
PD 07-OCT-1999.
XX
PF 26-MAR-1999; 99WO-US006641.
XX
PR 27-MAR-1998; 98US-0079751P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rybak SM, Newton DL;
XX
DR WPI; 1999-610847/52.
DR N-PSDB; AAZ08134.
XX
PT New recombinant ribonucleases, used for killing target cells, e.g. for
PT treating cancers, viral infections or autoimmune diseases.
XX
PS Claim 22; Page 67; 71pp; English.
XX
CC The present sequence is a recombinant Rana catesbeiana oocyte
CC ribonuclease (RaCOR1) protein with Gln1Ser. Carboxy terminal end of
CC recombinant RaCOR1 has a covalently bound ligand binding moiety, which
CC can be a LL2 antibody directed against CD22 on cancerous B cells or human
CC chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells.

```
RA   Beintema J.J.;
RT   "Secretory ribonuclease genes and pseudogenes in true ruminants.";
RL   Gene 212:259-268(1998).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y11670; CAA72368.1; -.
DR   HSSP; P00656; 1SRN.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT   ACT_SITE     41     41       BY SIMILARITY.
FT   DISULFID     26     84       BY SIMILARITY.
FT   DISULFID     40     95       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID     65     72       BY SIMILARITY.
FT   CARBOHYD     62     62       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   CARBOHYD    129    129       O-LINKED (BY SIMILARITY).
FT   CARBOHYD    133    133       O-LINKED (BY SIMILARITY).
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Qy         59 NVL----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHFA 105
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Db        122 G 122


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RN   [1]
RP   SEQUENCE.
RC   TISSUE=Milk, and Serum;
RX   MEDLINE=97409980; PubMed=9266695;
RA   Strydom D.J., Bond M.D., Vallee B.L.;
RT   "An angiogenic protein from bovine serum and milk -- purification and
RT   primary structure of angiogenin-2.";
RL   Eur. J. Biochem. 247:535-544(1997).
CC   -!- FUNCTION: Binds tightly to placental ribonuclease inhibitor and
CC       has very low ribonuclease activity. Has potent angiogenic
CC       activity. Angiogenin induces vascularization of normal and
CC       malignant tissues. Abolishes protein synthesis by specifically
CC       hydrolyzing cellular tRNAs.
CC   -!- TISSUE SPECIFICITY: Serum and milk.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR   HSSP; P10152; 1AGI.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Angiogenesis;
KW   Protein synthesis inhibitor; Glycoprotein;
KW   Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   ACT_SITE     12     12       BY SIMILARITY.
FT   ACT_SITE     39     39       BY SIMILARITY.
FT   ACT_SITE    113    113       BY SIMILARITY.
FT   DISULFID     25     80
FT   DISULFID     38     91
FT   DISULFID     56    106
FT   CARBOHYD     33     33       N-LINKED (GLCNAC. . .).
SQ   SEQUENCE   123 AA;  14522 MW;  B703B9839919FD2F CRC64;

  Query Match             20.4%;  Score 123.5;  DB 1;  Length 123;
  Best Local Similarity   29.6%;  Pred. No. 1.8e-06;
  Matches   32;  Conservative   20;  Mismatches   43;  Indels   13;  Gaps    5;

Qy          7 FQQKHIINTPI-----ICNTILDNNIYIVGGQCKRVNTFIISSATTVKAIC---TGVINL 58
              } :|| :|       |||:::    :  || ||||  ::  ::|:|    |
Db          8 FLRKHYDPSPTGHDDRYCNTMMERR--NMTRPCKDTNTFIHGNSDDIRAVCDDRNGEPYR 65

Qy         59 NVLSTTR--FQLNTCTRTSITPR-PCPYSSRTETNYICVKCENQYPVH 103
              | |  :|  ||: ||     :|| || | :      | ::| : :|:|
Db         66 NGLRRSRSPFQVTTCRHRGGSPRPPCRYRAFRANRVIVIRCRDGFPIH 113


RESULT 14
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ID   RNBR_GIRCA     STANDARD;      PRT;   141 AA.
AC   Q29542; Q29533;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ribonuclease, brain (EC 3.1.27.-) (BRB).
GN   BRN.
OS   Giraffa camelopardalis (Giraffe).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Giraffoidea;
OC   Giraffidae; Giraffa.
OX   NCBI_TaxID=9894;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96139017; PubMed=8587129;
RA   Confalone E., Beintema J.J., Sasso M.P., Carsana A., Palmieri M.,
RA   Vento M.T., Furia A.;
RT   "Molecular evolution of genes encoding ribonucleases in ruminant
RT   species.";
RL   J. Mol. Evol. 41:850-858(1995).
RN   [2]
RP   SEQUENCE OF 31-114 FROM N.A.
RX   MEDLINE=93367815; PubMed=8360916;
RA   Breukelman H.J., Beintema J.J., Confalone E., Costanzo C., Sasso M.P.,
RA   Carsana A., Palmieri M., Furia A.;
RT   "Sequences related to the ox pancreatic ribonuclease coding region in
RT   the genomic DNA of mammalian species.";
RL   J. Mol. Evol. 37:29-35(1993).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; S81743; AAB36137.1; -.
DR   EMBL; S65126; AAB27931.1; -.
DR   HSSP; P00656; 2RNS.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT   ACT_SITE     41     41       BY SIMILARITY.
FT   DISULFID     26     84       BY SIMILARITY.
FT   DISULFID     40     95       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID     65     72       BY SIMILARITY.
FT   CARBOHYD     62     62       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   CARBOHYD    129    129       O-LINKED (BY SIMILARITY).
SQ   SEQUENCE   141 AA;  15592 MW;  73745EFE9079591F CRC64;

  Query Match             20.4%;  Score 123.5;  DB 1;  Length 141;
  Best Local Similarity   29.8%;  Pred. No. 2.1e-06;
  Matches   36;  Conservative   18;  Mismatches   44;  Indels   23;  Gaps    7;

Qy          5 ATFQQKHI------INTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINL 58
              | |:::|:       :    || ::     :  |:|| ||||:  |   |||:|:
Db          6 AKFRRQHMDSGSSSSSNSNYCNQMMKRR-RMTHGRCKPVNTFVHESLADVKAVCS---QK 61

Qy         59 NVL----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHFA 105
              |:          | :   :  | |  :  | | | :  :  || | || | | ||||
Db         62 NITCKNGQPNCYQSNSTMNITDCRETGSSKYPNCAYKTSQKQKYITVACEGNPYVPVHFD 121

Qy        106 G 106
              |
Db        122 G 122


RESULT 15
RNBR_AXIPR
ID   RNBR_AXIPR     STANDARD;      PRT;   151 AA.
AC   P87350;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Ribonuclease, brain (EC 3.1.27.-) (BRB).
GN   BRN.
OS   Axis porcinus (Hog deer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC   Cervidae; Cervinae; Axis.
OX   NCBI_TaxID=57737;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98278842; PubMed=9611269;
RA   Breukelman H.J., van der Munnik N., Kleineidam R.G., Furia A.,
```

```
  Matches   37;  Conservative   18;  Mismatches   43;  Indels   23;  Gaps    7;

Qy          5 ATFQQKHI------INTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINL 58
              | |:::|:       : |  || ::     :  |:|| ||||:  |   |||:|:
Db         32 AKFRRQHMDSGSSSSSNPNYCNQMMKRR-RMTHGRCKPVNTFVHESLDDVKAVCS---QK 87

Qy         59 NVL----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHFA 105
              |:          | :  :  |  |  :  | | | :  :  || | || | | ||||
Db         88 NITCKNGHPNCYQSKSTMSITDCRETGSSKYPNCAYKTSQKQKYITVACEGNPYVPVHFD 147

Qy        106 G 106
              |
Db        148 G 148


RESULT 11
RNP_IGUIG
ID   RNP_IGUIG      STANDARD;      PRT;   119 AA.
AC   P80287;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
OS   Iguana iguana (Common iguana).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.
OX   NCBI_TaxID=8517;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Pancreas;
RX   MEDLINE=94139745; PubMed=8307028;
RA   Zhao W., Beintema J.J., Hofsteenge J.;
RT   "The amino acid sequence of iguana (Iguana iguana) pancreatic
RT   ribonuclease.";
RL   Eur. J. Biochem. 219:641-646(1994).
CC   -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC       phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC       with 2',3'-cyclic phosphate intermediates.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Pancreas.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR   PIR; S41111; S41111.
DR   HSSP; P00656; 1LSQ.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID     25     80       BY SIMILARITY.
FT   DISULFID     39     91       BY SIMILARITY.
FT   DISULFID     57    106       BY SIMILARITY.
FT   ACT_SITE     10     10       BY SIMILARITY.
FT   ACT_SITE     40     40       BY SIMILARITY.
FT   ACT_SITE    113    113       BY SIMILARITY.
SQ   SEQUENCE   119 AA;  13324 MW;  6072FB5B7B15BD5A CRC64;

  Query Match             21.1%;  Score 127.5;  DB 1;  Length 119;
  Best Local Similarity   29.6%;  Pred. No. 6.4e-07;
  Matches   34;  Conservative   17;  Mismatches   51;  Indels   13;  Gaps    4;

Qy          2 QNWATFQQKHI-------INTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAIC-- 52
              |:|::\\ \\\        |    |: ::     :   :||  |||: :| : :: :|
Db          1 QDWSSFQNKHIDYPETSASNPNAYCDLMMQRR-NLNPTKCKTRNTFVHASPSEIQQVCGS 59

Qy         53 --TGVINLNVLSTTRFQLNTCTRTSIT-PRPCPYSSRTETNYICVKCENQYPVHF 104
                |  :    |  | |  |     | |  | |:   |  | : |||  ||||
Db         60 GGTHYEDNLYDSNESFDLTDCKNVGGTAPSSCKYNGTPGTKRIRIACENNQPVHF 114


RESULT 12
RNBR_CAPCA
ID   RNBR_CAPCA      STANDARD;      PRT;   151 AA.
AC   P79351;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Ribonuclease, brain (EC 3.1.27.-) (BRB).
OS   Capreolus capreolus (Roe deer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC   Cervidae; Odocoileinae; Capreolus.
OX   NCBI_TaxID=9858;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98278842; PubMed=9611269;
RA   Breukelman H.J., van der Munnik N., Kleineidam R.G., Furia A.,
RA   Beintema J.J.;
RT   "Secretory ribonuclease genes and pseudogenes in true ruminants.";
RL   Gene 212:259-268(1998).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; Y11673; CAA72371.1; -.
DR   HSSP; P00656; 1SRN.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT   ACT_SITE     41     41       BY SIMILARITY.
FT   DISULFID     26     84       BY SIMILARITY.
FT   DISULFID     40     95       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID     65     72       BY SIMILARITY.
FT   CARBOHYD     62     62       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   CARBOHYD    129    129       O-LINKED (BY SIMILARITY).
FT   CARBOHYD    133    133       O-LINKED (BY SIMILARITY).
SQ   SEQUENCE   151 AA;  16971 MW;  392D0E6302F006A6 CRC64;

  Query Match             20.6%;  Score 124.5;  DB 1;  Length 151;
  Best Local Similarity   28.6%;  Pred. No. 1.7e-06;
  Matches   34;  Conservative   18;  Mismatches   44;  Indels   23;  Gaps    6;

Qy          5 ATFQQKHI------INTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINL 58
              | |:::|:       |  || ::     :  |:|| ||||:  |   |||:|:
Db          6 AKFRRQHMDSGSSSSGNPNYCNQMMKRR-RMTHGRCKPVNTFVHESLDNVKAVCS---QK 61

Qy         59 NVL----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCENQ--YPVHF 104
              |:          | :  :  | :|  :  | | | :  :  || | ||     ||||
Db         62 NITCKNGQPNCYQSNSTMNITDCRQTGSSKYPNCAYKTSQKQKYITVACEGDPYVPVHF 120


RESULT 13
ANG2_BOVIN
ID   ANG2_BOVIN     STANDARD;      PRT;   123 AA.
AC   P80929;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Angiogenin-2 (EC 3.1.27.-).
GN   ANG2.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
GN   RNASE1 OR RNS1.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=70104197; PubMed=5460946;
RA   Jackson R.L., Hirs C.H.W.;
RT   "The primary structure of porcine pancreatic ribonuclease. II. The
RT   amino acid sequence of the reduced S-aminoethylated protein.";
RL   J. Biol. Chem. 245:637-653(1970).
RN   [2]
RP   REVISION TO 2.
RA   Wierenga R.K., Huizinga J.D., Gaastra W., Welling G.W., Beintema J.J.;
RT   "Affinity chromatography of porcine pancreatic ribonuclease and
RT   reinvestigation of the N-terminal amino acid sequence.";
RL   FEBS Lett. 31:181-185(1973).
RN   [3]
RP   DISULFIDE BONDS.
RX   MEDLINE=70104198; PubMed=4904878;
RA   Phelan J.J., Hirs C.H.W.;
RT   "The primary structure of porcine pancreatic ribonuclease. 3. The
RT   disulfide bonds.";
RL   J. Biol. Chem. 245:654-661(1970).
CC   -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC       phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC       with 2',3'-cyclic phosphate intermediates.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Pancreas.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR   PIR; A92071; NRPG.
DR   HSSP; P00656; 1SRN.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT   DISULFID     26     84
FT   DISULFID     40     95
FT   DISULFID     58    110
FT   DISULFID     65     72
FT   ACT_SITE     12     12       BY SIMILARITY.
FT   ACT_SITE     41     41       BY SIMILARITY.
FT   ACT_SITE    119    119       BY SIMILARITY.
FT   CARBOHYD     21     21       N-LINKED (GLCNAC. . .).
FT   CARBOHYD     34     34       N-LINKED (GLCNAC. . .).
FT   CARBOHYD     76     76       N-LINKED (GLCNAC. . .).
SQ   SEQUENCE   124 AA;  13804 MW;  0AC28CDE14111845 CRC64;

  Query Match             21.4%;  Score 129.5;  DB 1;  Length 124;
  Best Local Similarity   30.7%;  Pred. No. 4.1e-07;
  Matches   35;  Conservative   20;  Mismatches   42;  Indels   17;  Gaps    6;

Qy          7 FQQKHI------INTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGV-INLN 59
              ||:|:|      |:   || ::     :  |:|| ||||:  |   |:|:|: : :|
Db          8 FQRQHMDPDSSSSNSSNYCNLMMSRR-NMTQGRCKPVNTFVHESLADVQAVCSQINVNCK 66

Qy         60 VLSTTRFQLNT------CTRTSITPRP-CPYSSRTETNYICVKCENQ--YPVHF 104
                 |  :| |:      | :|  :  | | | :  |  :| | ||     ||||
Db         67 NGQTNCYQSNSTMHITDCRQTGSSKYPNCAYKASQEQKHIIVACEGNPPVPVHF 120


RESULT 10
RNBR_BOVIN
ID   RNBR_BOVIN     STANDARD;      PRT;   167 AA.
AC   P39873;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ribonuclease, brain precursor (EC 3.1.27.-) (BRB).
GN   BRN.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92093604; PubMed=1754384;
RA   Sasso M.P., Carsana A., Confalone E., Cosi C., Sorrentino S.,
RA   Viola M., Palmieri M., Russo E., Furia A.;
RT   "Molecular cloning of the gene encoding the bovine brain ribonuclease
RT   and its expression in different regions of the brain.";
RL   Nucleic Acids Res. 19:6469-6474(1991).
RN   [2]
RP   SEQUENCE OF 27-167, AND CARBOHYDRATE-LINKAGE SITES.
RC   TISSUE=Brain;
RX   MEDLINE=89214015; PubMed=3243767;
RA   Watanabe H., Katoh H., Ishii M., Komoda Y., Sanda A., Takizawa Y.,
RA   Ohgi K., Irie M.;
RT   "Primary structure of a ribonuclease from bovine brain.";
RL   J. Biochem. 104:939-945(1988).
RN   [3]
RP   SEQUENCE OF 27-167 FROM N.A.
RX   MEDLINE=96139017; PubMed=8587129;
RA   Confalone E., Beintema J.J., Sasso M.P., Carsana A., Palmieri M.,
RA   Vento M.T., Furia A.;
RT   "Molecular evolution of genes encoding ribonucleases in ruminant
RT   species.";
RL   J. Mol. Evol. 41:850-858(1995).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X59767; CAA42439.1; -.
DR   EMBL; S81744; AAB36138.1; -.
DR   PIR; S20066; S20066.
DR   HSSP; P00656; 2RNS.
DR   GlycoSuiteDB; P39873; -.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Glycoprotein; Signal.
FT   SIGNAL        1     26
FT   CHAIN        27    167       RIBONUCLEASE, BRAIN.
FT   ACT_SITE     38     38       BY SIMILARITY.
FT   ACT_SITE     67     67       BY SIMILARITY.
FT   ACT_SITE    145    145       BY SIMILARITY.
FT   DISULFID     52    110       BY SIMILARITY.
FT   DISULFID     66    121       BY SIMILARITY.
FT   DISULFID     84    136       BY SIMILARITY.
FT   DISULFID     91     98       BY SIMILARITY.
FT   CARBOHYD     88     88       N-LINKED (GLCNAC. . .).
FT                                /FTId=CAR_000005.
FT   CARBOHYD    155    155       O-LINKED.
FT   CARBOHYD    159    159       O-LINKED.
FT   CONFLICT    155    155       T -> S (IN REF. 2).
SQ   SEQUENCE   167 AA;  18450 MW;  681CAAC3CC2FC459 CRC64;

  Query Match             21.4%;  Score 129.5;  DB 1;  Length 167;
  Best Local Similarity   30.6%;  Pred. No. 5.6e-07;
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```
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   PARTIAL SEQUENCE.
RC   TISSUE=Serum;
RX   MEDLINE=93192291; PubMed=8448182;
RA   Bond M.D., Strydom D.J., Vallee B.L.;
RT   "Characterization and sequencing of rabbit, pig and mouse
RT   angiogenins: discernment of functionally important residues and
RT   regions.";
RL   Biochim. Biophys. Acta 1162:177-186(1993).
CC   -!- FUNCTION: May function as a tRNA-specific ribonuclease that binds
CC       to actin on the surface of endothelial cells; once bound,
CC       angiogenin is endocytosed and translocated to the nucleus, thereby
CC       promoting the endothelial invasiveness necessary for blood vessel
CC       formation. Angiogenin induces vascularization of normal and
CC       malignant tissues. Abolishes protein synthesis by specifically
CC       hydrolyzing cellular tRNAs.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC   ----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U22516; AAA91366.1; -.
DR   EMBL; BC055355; AAH55355.1; -.
DR   PIR; A35932; A35932.
DR   HSSP; P03950; 1A4Y.
DR   MGD; MGI:88022; Ang.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Angiogenesis;
KW   Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
FT   SIGNAL       1     24
FT   CHAIN       25    145       ANGIOGENIN.
FT   MOD_RES      25     25       PYRROLIDONE CARBOXYLIC ACID (BY
FT                                SIMILARITY).
FT   ACT_SITE     37     37       BY SIMILARITY.
FT   ACT_SITE     64     64       BY SIMILARITY.
FT   ACT_SITE    137    137       BY SIMILARITY.
FT   DISULFID     50    104       BY SIMILARITY.
FT   DISULFID     63    115       BY SIMILARITY.
FT   DISULFID     81    130       BY SIMILARITY.
SQ   SEQUENCE   145 AA;  16228 MW;  06944260BB764938 CRC64;

  Query Match             22.6%;  Score 136.5;  DB 1;  Length 145;
  Best Local Similarity   40.3%;  Pred. No. 8.4e-08;
  Matches   31;  Conservative   11;  Mismatches   28;  Indels    7;  Gaps    3;

Qy         34 CKRVNTFIISSATTVKAICTG-----VINLNVLSTTRFQLNTCTRTSITPR-PCPYSSRT 87
               || |||||  : : :||||         ||  :| : ||: ||  |  :|| || | :
Db         63 CKDVNTFIHGNKSNIKAICGANGSPYRENLR-MSKSPFQVTTCKHTGGSPRPPCQYRASA 121

Qy         88 ETNYICVKCENQYPVHF 104
                 :: : |||  ||||
Db        122 GFRHVVIACENGLPVHF 138


RESULT 8
RNP_BALAC
ID   RNP_BALAC      STANDARD;      PRT;   124 AA.
AC   P00673;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
GN   RNASE1 OR RNS1.
OS   Balaenoptera acutorostrata (Minke whale) (Lesser rorqual).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
OC   Balaenopteridae; Balaenoptera.
OX   NCBI_TaxID=9767;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76277855; PubMed=962870;
RA   Emmens M., Welling G.W., Beintema J.J.;
RT   "The amino acid sequence of pike-whale (lesser-rorqual) pancreatic
RT   ribonuclease.";
RL   Biochem. J. 157:317-323(1976).
CC   -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC       phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC       with 2',3'-cyclic phosphate intermediates.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Pancreas.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR   PIR; A00818; NRWHK.
DR   HSSP; P00656; 1SRN.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT   DISULFID     26     84       BY SIMILARITY.
FT   DISULFID     40     95       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID     65     72       BY SIMILARITY.
FT   ACT_SITE     12     12       BY SIMILARITY.
FT   ACT_SITE     41     41       BY SIMILARITY.
FT   ACT_SITE    119    119       BY SIMILARITY.
FT   CARBOHYD     76     76       N-LINKED (GLCNAC. . .) (30%).
SQ   SEQUENCE   124 AA;  14125 MW;  F57475459F697E20 CRC64;

  Query Match             21.7%;  Score 131.5;  DB 1;  Length 124;
  Best Local Similarity   32.5%;  Pred. No. 2.5e-07;
  Matches   38;  Conservative   17;  Mismatches   39;  Indels   23;  Gaps    7;

Qy          7 FQQKHII------NTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 60
              ||::|:       | |  || ::     :  |:|| ||||:  |   |||:|:      ||
Db          8 FQRQHMDSGNSPGNNPNYCNQMMMRR-KMTQGRCKPVNTFVHESLEDVKAVCS---QKNV 63

Qy         61 L----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 104
              |          | :   :  | :|  :  | | | :  :  :| | || | | ||||
Db         64 LCKNGRTNCYESNSTMHITDCRQTGSSKYPNCAYKTSQKEKHIIVACEGNPYVPVHF 120


RESULT 9
RNP_PIG
ID   RNP_PIG        STANDARD;      PRT;   124 AA.
AC   P00671;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
```

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RT   developmentally regulated genes when expressed in NIH 3T3
RT   fibroblasts.";
RL   Mol. Cell. Biol. 17:1503-1512(1997).
CC   -!- FUNCTION: Angiogenin induces vascularization of normal and
CC       malignant tissues. Abolishes protein synthesis by specifically
CC       hydrolyzing cellular tRNAs (By similarity).
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U72672; AAC05794.1; -.
DR   HSSP; P10152; 1AGI.
DR   MGD; MGI:1201793; Angl.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Angiogenesis;
KW   Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
FT   SIGNAL        1     24       POTENTIAL.
FT   CHAIN        25    145       ANGIOGENIN-3.
FT   MOD_RES      25     25       PYRROLIDONE CARBOXYLIC ACID
FT                                (BY SIMILARITY).
FT   ACT_SITE     37     37       BY SIMILARITY.
FT   ACT_SITE     64     64       BY SIMILARITY.
FT   ACT_SITE    137    137       BY SIMILARITY.
FT   DISULFID     50    104       BY SIMILARITY.
FT   DISULFID     63    115       BY SIMILARITY.
FT   DISULFID     81    130       BY SIMILARITY.
SQ   SEQUENCE   145 AA;  16696 MW;  DE9D3BC92F1D682C CRC64;

  Query Match             25.5%;  Score 154.5;  DB 1;  Length 145;
  Best Local Similarity   43.6%;  Pred. No. 9.7e-10;
  Matches   34;  Conservative   12;  Mismatches   23;  Indels    9;  Gaps    4;

Qy         34 CKRVNTFIISSATTVKAIC------TGVINLNVLSTTRFQLNTCTRTSITPR-PCPYSSR 86
              || |||||  :   :||||       || |  : | :|||: |||    :|| || |::
Db         63 CKEVNTFIHDTKNNIKAICGENGRPYGV-NFRI-SNSRFQVTTCTHKGGSPRPPCQYNAF 120

Qy         87 TETNYICVKCENQYPVHF 104
                 :  || : ||: :||||
Db        121 KDFRYIVIACEDGWPVHF 138


RESULT 6
ANGR_MOUSE
ID   ANGR_MOUSE     STANDARD;      PRT;   145 AA.
AC   Q64438;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Angiogenin-related protein precursor.
GN   ANGRP.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129; TISSUE=Liver;
RX   MEDLINE=96079109; PubMed=8530072;
RA   Brown W.E., Nobile V., Subramanian V., Shapiro R.;
RT   "The mouse angiogenin gene family: structures of an angiogenin-related
RT   protein gene and two pseudogenes.";
RL   Genomics 29:200-206(1995).
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U22519; AAA91367.1; -.
DR   HSSP; P03950; 1A4Y.
DR   MGD; MGI:104984; Angrp.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal; Hydrolase; Nuclease; Endonuclease;
KW   Pyrrolidone carboxylic acid.
FT   SIGNAL        1     24       POTENTIAL.
FT   CHAIN        25    145       ANGIOGENIN-RELATED PROTEIN.
FT   MOD_RES      25     25       PYRROLIDONE CARBOXYLIC ACID (BY
FT                                SIMILARITY).
FT   ACT_SITE     37     37       BY SIMILARITY.
FT   ACT_SITE     64     64       BY SIMILARITY.
FT   ACT_SITE    137    137       BY SIMILARITY.
FT   DISULFID     50    104       BY SIMILARITY.
FT   DISULFID     63    115       BY SIMILARITY.
FT   DISULFID     81    130       BY SIMILARITY.
SQ   SEQUENCE   145 AA;  16612 MW;  29A6EB814429C4AD CRC64;

  Query Match             24.7%;  Score 149.5;  DB 1;  Length 145;
  Best Local Similarity   44.2%;  Pred. No. 3.4e-09;
  Matches   34;  Conservative    9;  Mismatches   27;  Indels    7;  Gaps    3;

Qy         34 CKRVNTFIISSATTVKAICTGV-----INLNVLSTTRFQLNTCTRTSITPR-PCPYSSRT 87
              || |||||  :   :||||          || : | :|||: |||    :|| || | :
Db         63 CKDVNTFIHDTKNNIKAICGKKGSPYGRNLRI-SKSRFQVTTCTHKGRSPRPPCRYRASK 121

Qy         88 ETNYICVKCENQYPVHF 104
                 || : ||| :||||
Db        122 GFRYIIIGCENGWPVHF 138


RESULT 7
ANGI_MOUSE
ID   ANGI_MOUSE     STANDARD;      PRT;   145 AA.
AC   P21570;
DT   01-MAY-1991 (Rel. 18, Created)
DT   01-MAY-1991 (Rel. 18, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).
GN   ANG.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91025023; PubMed=2222458;
RA   Bond M.D., Vallee B.L.;
RT   "Isolation and sequencing of mouse angiogenin DNA.";
RL   Biochem. Biophys. Res. Commun. 171:988-995(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Liver;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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RL   J. Biochem. 106:729-735(1989).
CC   -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC       phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC       with 2',3'-cyclic phosphate intermediates.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR   PIR; JX0085; JX0085.
DR   HSSP; P11916; 1BC4.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   ACT_SITE     10     10       BY SIMILARITY.
FT   ACT_SITE     35     35       BY SIMILARITY.
FT   ACT_SITE    104    104       BY SIMILARITY.
FT   DISULFID     19     72       BY SIMILARITY.
FT   DISULFID     34     82       BY SIMILARITY.
FT   DISULFID     52     97       BY SIMILARITY.
FT   DISULFID     94    111       PROBABLE.
SQ   SEQUENCE   111 AA;  12461 MW;  D64BA72456C10788 CRC64;

  Query Match             61.2%;  Score 370;  DB 1;  Length 111;
  Best Local Similarity   64.9%;  Pred. No. 4.4e-33;
  Matches   72;  Conservative   10;  Mismatches   27;  Indels    2;  Gaps    2;

Qy          2 QNWATFQQKHIINTPII-CNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 59
              |||| |::||| :|  | ||||:|  ||||||:||  |||||||   |||||:||  :
Db          1 QNWAKFKEKHIRSTSSIDCNTIMDKAIYIVGGKCKERNTFIISSEDNVKAICSGVSPDRK 60

Qy         60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                |||| |:|||| | |||||||||    : | |||||| | |||| |||:|
Db         61 ELSTTSFKLNTCIRDSITPRPCPYHPSPDNNKICVKCEKQLPVHFVGIGKC 111


RESULT 4
RN30_RANPI
ID   RN30_RANPI     STANDARD;      PRT;   104 AA.
AC   P22069;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   P-30 protein (EC 3.1.27.-) (Onconase).
OS   Rana pipiens (Northern leopard frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8404;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Embryo;
RX   MEDLINE=91093131; PubMed=1985896;
RA   Ardelt W., Mikulski S.M., Shogen K.;
RT   "Amino acid sequence of an anti-tumor protein from Rana pipiens
RT   oocytes and early embryos. Homology to pancreatic ribonucleases.";
RL   J. Biol. Chem. 266:245-251(1991).
RN   [2]
RP   3D-STRUCTURE MODELING.
RX   MEDLINE=93066156; PubMed=1438177;
RA   Mosimann S.C., Johns K.L., Ardelt W., Mikulski S.M., Shogen K.,
RA   James M.N.G.;
RT   "Comparative molecular modeling and crystallization of P-30 protein:
RT   a novel antitumor protein of Rana pipiens oocytes and early
RT   embryos.";
RL   Proteins 14:392-400(1992).
RN   [3]
RP   X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
RX   MEDLINE=94166079; PubMed=8120892;
RA   Mosimann S.C., Ardelt W., James M.N.G.;
RT   "Refined 1.7 A X-ray crystallographic structure of P-30 protein, an
RT   amphibian ribonuclease with anti-tumor activity.";
RL   J. Mol. Biol. 236:1141-1153(1994).
CC   -!- FUNCTION: Basic protein with antiproliferative/cytotoxic activity
CC       against several tumor cell lines in vitro, as well as antitumor
CC       in vivo. It exhibits a ribonuclease-like activity against high
CC       molecular weight ribosomal RNA.
CC   -!- DEVELOPMENTAL STAGE: Early embryos (up to four blastomere stage).
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR   PDB; 1ONC; 31-JAN-94.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; 3D-structure;
KW   Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   ACT_SITE     10     10
FT   ACT_SITE     31     31
FT   ACT_SITE     97     97
FT   DISULFID     19     68
FT   DISULFID     30     75
FT   DISULFID     48     90
FT   DISULFID     87    104
FT   HELIX         3     10
FT   STRAND       11     12
FT   HELIX        19     22
FT   TURN         23     24
FT   TURN         26     30
FT   STRAND       33     38
FT   HELIX        41     45
FT   HELIX        46     48
FT   TURN         49     50
FT   STRAND       55     58
FT   STRAND       63     70
FT   TURN         74     75
FT   STRAND       77     84
FT   STRAND       86     91
FT   TURN         92     93
FT   STRAND       94    101
SQ   SEQUENCE   104 AA;  11845 MW;  22A753C2F9E566B4 CRC64;

  Query Match             45.2%;  Score 273.5;  DB 1;  Length 104;
  Best Local Similarity   48.6%;  Pred. No. 1e-22;
  Matches   54;  Conservative   16;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          2 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 59
              |:| |||:||| ||  : |: |:  |::     ||  |||| |    ||||| |:| : |
Db          1 QDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56

Qy         60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104


RESULT 5
ANG3_MOUSE
ID   ANG3_MOUSE     STANDARD;      PRT;   145 AA.
AC   P97802;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Angiogenin-3 precursor (EC 3.1.27.-) (Angiogenin-related protein 2)
DE   (EF-5).
GN   ANG3 OR ANGL.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RX   MEDLINE=97184476; PubMed=9032278;
RA   Fu X., Kamps M.P.;
RT   "E2a-Pbx1 induces aberrant expression of tissue-specific and
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CC       residues with a 3'flanking guanine. Hydrolyzes poly(U) and poly(C)
CC       as substrates, and prefers the former. The S-lectins in frog eggs
CC       may be involved in the fertilization and development of the frog
CC       embryo. This lectin agglutinates various animal cells, including
CC       normal lymphocytes, erythrocytes, and fibroblasts of animal and
CC       human origin. It is cytotoxic against several tumor cells.
CC   -!- SUBUNIT: Monomer.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF039104; AAD10702.1; -.
DR   PIR; A27121; A27121.
DR   PDB; 1BC4; 28-OCT-98.
DR   PDB; 1M07; 21-JAN-03.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure;
KW   Signal; Pyrrolidone carboxylic acid.
FT   SIGNAL       1     22
FT   CHAIN       23    133       RIBONUCLEASE, OOCYTES.
FT   MOD_RES     23     23       PYRROLIDONE CARBOXYLIC ACID.
FT   ACT_SITE    32     32
FT   ACT_SITE    57     57
FT   ACT_SITE   125    125
FT   DISULFID    41     93
FT   DISULFID    56    103
FT   DISULFID    74    118
FT   DISULFID   115    132
FT   HELIX       25     32
FT   HELIX       41     45
FT   TURN        48     49
FT   STRAND      59     63
FT   HELIX       67     73
FT   TURN        74     74
FT   STRAND      79     84
FT   STRAND      90     95
FT   STRAND     105    110
FT   STRAND     114    119
FT   TURN       120    121
FT   STRAND     122    129
SQ   SEQUENCE   133 AA;  14762 MW;  A7D62594F7D16F0C CRC64;

  Query Match             96.8%;  Score 585.5;  DB 1;  Length 133;
  Best Local Similarity   97.3%;  Pred. No. 3.2e-56;
  Matches  108;  Conservative    2;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          2 QNWATFQQKHIINTPII-CNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 60
              |||||||||||||||||| |||||:|||||||||||||||||||||||||||||||:||
Db         23 QNWATFQQKHIINTPIINCNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 82

Qy         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 133


RESULT 2
LECS_RANJA
ID   LECS_RANJA     STANDARD;      PRT;   111 AA.
AC   P18839;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Sialic acid-binding lectin (EC 3.1.27.-).
OS   Rana japonica (Japanese reddish frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8402;
RN   [1]
RP   SEQUENCE, AND DISULFIDE BONDS.
RC   TISSUE=Egg;
RX   MEDLINE=91035319; PubMed=2229005;
RA   Kamiya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawauchi H.,
RA   Takayanagi Y., Titani K.;
RT   "Amino acid sequence of a lectin from Japanese frog (Rana japonica)
RT   eggs.";
RL   J. Biochem. 108:139-143(1990).
CC   -!- FUNCTION: The S-lectins in frog eggs may be involved in the
CC       fertilization and development of the frog embryo. This lectin
CC       preferentially agglutinate a large variety of tumor cells, but it
CC       does not agglutinate non-transformed cells and erythrocytes.
CC   -!- SUBUNIT: Monomer.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR   PIR; JX0120; JX0120.
DR   HSSP; P11916; 1BC4.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin;
KW   Pyrrolidone carboxylic acid.
FT   MOD_RES      1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   ACT_SITE    10     10       BY SIMILARITY.
FT   ACT_SITE    35     35       BY SIMILARITY.
FT   ACT_SITE   104    104       BY SIMILARITY.
FT   DISULFID    19     72
FT   DISULFID    34     82
FT   DISULFID    52     97
FT   DISULFID    94    111
SQ   SEQUENCE   111 AA;  12326 MW;  FDEBDDF3834ED679 CRC64;

  Query Match             74.5%;  Score 451;  DB 1;  Length 111;
  Best Local Similarity   77.5%;  Pred. No. 8.1e-42;
  Matches   86;  Conservative    8;  Mismatches   15;  Indels    2;  Gaps    2;

Qy          2 QNWATFQQKHIINTP-IICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGV-INLN 59
              |||| ||:||| ||  | ||||:| :||||||||| ||||||||||||||:|  | |
Db          1 QNWAKFQEKHIPNTSNINCNTIMDKSIYIVGGQCKERNTFIISSATTVKAICSGASTNRN 60

Qy         60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              |||||||||||| |::  |||||:|||||| |||||||: ||||||||||
Db         61 VLSTTRFQLNTCIRSATAPRPCPYNSRTETNVICVKCENRLPVHFAGIGRC 111


RESULT 3
RNPL_RANCA
ID   RNPL_RANCA     STANDARD;      PRT;   111 AA.
AC   P14626;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Ribonuclease, liver (EC 3.1.27.5).
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Liver;
RX   MEDLINE=90130374; PubMed=2613682;
RA   Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,
RA   Okazaki T., Ohgi K., Irie M.;
RT   "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana)
RT   liver.";
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 7, 2004, 21:30:40 ; Search time 5.60711 Seconds
(without alignments)
1030.796 Million cell updates/sec

Title: US-09-961-400-21
Perfect score: 605
Sequence: 1 MQNWATFQQKHIINTPIICN.....ICVKCENQYPVHFAGIGRCP 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	585.5	96.8	133	1	RNPO_RANCA	P11916 rana catesb
2	451	74.5	111	1	LECS_RANJA	P18839 rana japoni
3	370	61.2	111	1	RNPL_RANCA	P14626 rana catesb
4	273.5	45.2	104	1	RN30_RANPI	P22069 rana pipien
5	154.5	25.5	145	1	ANG3_MOUSE	P97802 mus musculu
6	149.5	24.7	145	1	ANGR_MOUSE	Q64438 mus musculu
7	136.5	22.6	145	1	ANGI_MOUSE	P21570 mus musculu
8	131.5	21.7	124	1	RNP_BALAC	P00673 balaenopter
9	129.5	21.4	124	1	RNP_PIG	P00671 sus scrofa
10	129.5	21.4	167	1	RNBR_BOVIN	P39873 bos taurus
11	127.5	21.1	119	1	RNP_IGUIG	P80287 iguana igua
12	124.5	20.6	151	1	RNBR_CAPCA	P79351 capreolus c
13	123.5	20.4	123	1	ANG2_BOVIN	P80929 bos taurus
14	123.5	20.4	141	1	RNBR_GIRCA	Q29542 giraffa cam
15	123.5	20.4	151	1	RNBR_AXIPR	P87350 axis porcin
16	123	20.3	146	1	ANGI_MIOTA	Q8wn65 miopithecus
17	123	20.3	146	1	ANGI_SAISC	Q8wn60 saimiri sci
18	120	19.8	146	1	ANGI_CERAE	Q8wn66 cercopithec
19	120	19.8	147	1	ANGI_PONPY	Q8wn67 pongo pygma
20	119.5	19.8	143	1	RNBR_SHEEP	Q29543 ovis aries
21	119	19.7	122	1	RNP_MACRU	P00686 macropus ru
22	118.5	19.6	123	1	ANGI_PIG	P31346 sus scrofa
23	118.5	19.6	124	1	RNP_ANTAM	P00668 antilocapra
24	118	19.5	146	1	ANGI_AOTTR	Q8wn61 aotus trivi
25	117	19.3	146	1	ANGI_SAGOE	Q8wn62 saguinus oe
26	116.5	19.3	128	1	RNP_MYOCO	P00676 myocastor c
27	116.5	19.3	149	1	RNP_MOUSE	P00683 mus musculu
28	115	19.0	146	1	ANGI_MACMU	Q8wn63 macaca mula
29	114.5	18.9	128	1	RNPB_CAVPO	P00679 cavia porce
30	114	18.8	148	1	ANGI_BOVIN	P10152 bos taurus
31	113.5	18.8	124	1	RNP_CAMDR	P00670 camelus dro
32	113.5	18.8	128	1	RNP_HORSE	P00674 equus cabal
33	113	18.7	147	1	ANGI_HUMAN	P03950 homo sapien
34	113	18.7	147	1	ANGI_PANTR	Q8wme8 *pan troglod*
35	112.5	18.6	119	1	RNS4_BOVIN	P15467 bos taurus
36	112.5	18.6	128	1	RNP_PROGU	P04059 proechimys
37	109.5	18.1	124	1	RNP_RANTA	P00666 rangifer ta
38	109.5	18.1	146	1	ANGI_PAPHA	Q8wn64 papio hamad
39	109.5	18.1	148	1	RNS4_MOUSE	Q9jjh1 mus musculu
40	109	18.0	125	1	ANGI_RABIT	P31347 oryctolagus
41	108.5	17.9	124	1	RNP_CAPCA	P00664 capreolus c
42	108.5	17.9	124	1	RNP_GIRCA	P00662 giraffa cam
43	108.5	17.9	130	1	RNP_CRILO	P24717 cricetulus
44	107.5	17.8	124	1	RNP_BUBBU	P00657 bubalus bub
45	107.5	17.8	148	1	RNP_PERLE	Q9wuv5 peromyscus

ALIGNMENTS

RESULT 1
RNPO_RANCA
ID RNPO_RANCA STANDARD; PRT; 133 AA.
AC P11916; Q9PWR7;
DT 01-OCT-1989 (Rel. 12, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ribonuclease, oocytes precursor (EC 3.1.27.-) (RC-RNase) (Sialic acid-
DE binding lectin) (SBL-C).
GN RCR.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98165825; PubMed=9497370;
RA Huang H.C., Wang S.C., Leu Y.J., Lu S.C., Liao Y.D.;
RT "The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease.
RT Tissue distribution, cloning, purification, cytotoxicity, and active
RT residues for RNase activity.";
RL J. Biol. Chem. 273:6395-6401(1998).
RN [2]
RP SEQUENCE OF 23-133.
RC TISSUE=Egg;
RX MEDLINE=87299649; PubMed=3304421;
RA Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H.,
RA Takayanagi G., Hakomori S.;
RT "Amino acid sequence of sialic acid binding lectin from frog (Rana
RT catesbeiana) eggs.";
RL Biochemistry 26:2189-2194(1987).
RN [3]
RP CHARACTERIZATION, AND SEQUENCE OF 81-101.
RX MEDLINE=92220613; PubMed=1373237;
RA Liao Y.-D.;
RT "A pyrimidine-guanine sequence-specific ribonuclease from Rana
RT catesbeiana (bullfrog) oocytes.";
RL Nucleic Acids Res. 20:1371-1377(1992).
RN [4]
RP CHARACTERIZATION.
RC TISSUE=Egg;
RX MEDLINE=93192604; PubMed=8448385;
RA Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawauchi H.,
RA Takayanagi Y., Hakomori S., Titani K.;
RT "Ribonuclease activity of sialic acid-binding lectin from Rana
RT catesbeiana eggs.";
RL Glycobiology 3:37-45(1993).
RN [5]
RP STRUCTURE BY NMR OF 23-133.
RX MEDLINE=98437383; PubMed=9761686;
RA Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;
RT "The solution structure of a cytotoxic ribonuclease from the oocytes
RT of Rana catesbeiana (bullfrog).";
RL J. Mol. Biol. 283:231-244(1998).
CC -!- FUNCTION: Preferentially cleaves single-stranded RNA at pyrimidine

```
Qy          7 FQQKHI------INTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 60
              ||::|:      ||:|  || ::     :  | || ||||:      |:|:|:     ||
Db         33 FQRQHMDPDGSSINSPTYCNQMMKRR-DMTNGSCKPVNTFVHEPLADVQAVCS---QENV 88

Qy         61 L----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 104
                        |::   :  |     :  | | | :     :| | || | | ||||
Db         89 TCKNRKSNCYKSSSALHITDCHLKGNSKYPNCDYKTTQYQKHIIVACEGNPYVPVHF 145


RESULT 15
NRGPB
pancreatic ribonuclease (EC 3.1.27.5) B - guinea pig (tentative sequence)
N;Alternate names: RNase IB
C;Species: Cavia porcellus (guinea pig)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C;Accession: A00826
R;van den Berg, A.; van den Hende-Timmer, L.; Hofsteenge, J.; Gaastra, W.; Beintema, J.J
Eur. J. Biochem. 75, 91-100, 1977
A;Title: Guinea pig pancreatic ribonucleases. Isolation, properties, primary structure a
A;Reference number: A91247; MUID:77185023; PMID:862624
A;Accession: A00826
A;Molecule type: protein
A;Residues: 1-128 <VAN>
A;Note: 64-Pro was also found
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;21,34/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted

  Query Match             18.9%;  Score 114.5;  DB 1;  Length 128;
  Best Local Similarity   30.8%;  Pred. No. 0.00024;
  Matches   36;  Conservative   15;  Mismatches   43;  Indels   23;  Gaps    6;

Qy          7 FQQKHI------INTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 60
              ||::|:       |:   || ::     :  |:|| ||||:  |   |:|:|      ||
Db          8 FQRQHMDPEGSPSNSSNYCNVMMIRR-NMTQGRCKPVNTFVHESLADVQAVC---FQKNV 63

Qy         61 L----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCENQ--YPVHF 104
              |          | :| ::  |  || :  | | |         | | ||    ||||
Db         64 LCKNGQTNCYQSYSRMRITDCRVTSSSKFPNCSYRMSQAQKSIIVACEGDPYVPVHF 120


Search completed: May  7, 2004, 21:54:56
Job time : 10.072 secs
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Db          7 FQRQHMDTEHSTASSSNYCNLMMKAR-DMTSGRCKPLNTFIHEPKSVVDAVCHQENVTCK 65

Qy         53 TGVINLNVLSTTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCENQY-PVHF 104
              |  |    | :|  :  | :|  :  | | | :      | | || || ||||
Db         66 NGRTNC-YKSNSRLSITNCRQTGASKYPNCQYETSNLNKQIIVACEGQYVPVHF 118


RESULT 11
A43825
angiogenin - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S29834; A43825
R;Bond, M.D.; Strydom, D.J.; Vallee, B.L.
Biochim. Biophys. Acta 1162, 177-186, 1993
A;Title: Characterization and sequencing of rabbit, pig and mouse angiogenins: discernme
A;Reference number: S29833; MUID:93192291; PMID:8448182
A;Accession: S29834
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-123 <BON>
A;Note: this sequence was submitted to the Protein Sequence Database, December 1992
C;Superfamily: pancreatic ribonuclease

  Query Match             19.6%;  Score 118.5;  DB 1;  Length 123;
  Best Local Similarity   39.5%;  Pred. No. 9.2e-05;
  Matches   30;  Conservative    6;  Mismatches   35;  Indels    5;  Gaps    2;

Qy         34 CKRVNTFIISSATTVKAICTG----VINLNVLSTTRFQLNTCTRTSITPR-PCPYSSRTE 88
              || |||||  :   :||||        |    | : ||: ||     : | || | :
Db         39 CKEVNTFIHGTRNDIKAICNDKNGEPYNNFRRSKSPFQITTCKHKGGSNRPPCGYRATAG 98

Qy         89 TNYICVKCENQYPVHF 104
                | | |||  ||||
Db         99 FRTIAVACENGLPVHF 114


RESULT 12
NRPRH
pancreatic ribonuclease (EC 3.1.27.5) - pronghorn (tentative sequence)
N;Alternate names: RNase 1; RNase A
C;Species: Antilocapra americana (pronghorn)
C;Date: 28-Feb-1981 #sequence_revision 28-Feb-1981 #text_change 31-Mar-2000
C;Accession: A00813
R;Beintema, J.J.; Gaastra, W.; Munniksma, J.
J. Mol. Evol. 13, 305-316, 1979
A;Title: Primary structure of pronghorn pancreatic ribonuclease: close relationship betw
A;Reference number: A00813; MUID:80075014; PMID:513141
A;Accession: A00813
A;Molecule type: protein
A;Residues: 1-124 <BEI>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F;34/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

  Query Match             19.6%;  Score 118.5;  DB 1;  Length 124;
  Best Local Similarity   29.9%;  Pred. No. 9.3e-05;
  Matches   35;  Conservative   19;  Mismatches   44;  Indels   19;  Gaps    7;

Qy          5 ATFQQKHIINTPI------ICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICT----- 53
              | |:::|| : |        || :: :   :  |:|| ||||:  |   |:|:|:
Db          6 AKFERQHIDSNPSSVSSSNYCNQMMKSR-NLTQGRCKPVNTFVHESLADVQAVCSQKNVA 64

Qy         54 ---GVINLNVLSTTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 104
                |  |    | :   :  |  |  :  | | | :     :| | || | | |||:
Db         65 CKNGQTNC-YQSYSTMSITDCRETGSSKYPNCAYKTTQAKKHIIVACEGNPYVPVHY 120


RESULT 13
NRCU
pancreatic ribonuclease (EC 3.1.27.5) - nutria (tentative sequence)
N;Alternate names: RNase 1; RNase A
C;Species: Myocastor coypus (nutria, coypu)
C;Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
C;Accession: A00822
R;van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
Biochim. Biophys. Acta 453, 400-409, 1976
A;Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic r
A;Reference number: A90612; MUID:77065676; PMID:999896
A;Accession: A00822
A;Molecule type: protein
A;Residues: 1-128 <VAN>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F;34/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match             19.3%;  Score 116.5;  DB 1;  Length 128;
  Best Local Similarity   30.8%;  Pred. No. 0.00015;
  Matches   36;  Conservative   16;  Mismatches   42;  Indels   23;  Gaps    7;

Qy          7 FQQKHI------INTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 60
              |:::|:          |  || :: :   :  |:|| ||||:      |:|:|      ||
Db          8 FERQHMDSRGSPSTNPNYCNEMMKSR-NMTQGRCKPVNTFVHEPLADVQAVC---FQKNV 63

Qy         61 L----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 104
              |          | :   :  |  || :  | | | :   |    | | || | | ||||
Db         64 LCKNGQTNCYQSNSNMHITDCRVTSNSDYPNCSYRTSQEEKSIVVACEGNPYVPVHF 120


RESULT 14
NRMS
pancreatic ribonuclease (EC 3.1.27.5) precursor - mouse
N;Alternate names: RNase 1; RNase A
C;Species: Mus musculus (house mouse)
C;Date: 30-Nov-1980 #sequence_revision 13-Mar-1997 #text_change 18-Jun-1999
C;Accession: A34090; S22598; A00830
R;Schueller, C.; Nijssen, H.M.J.; Kok, R.; Beintema, J.J.
Mol. Biol. Evol. 7, 29-44, 1990
A;Title: Evolution of nucleic acids coding for ribonucleases: the mRNA sequence of mouse
A;Reference number: A34090; MUID:90136034; PMID:2299980
A;Accession: A34090
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-149 <SCH>
A;Cross-references: GB:M27814; NID:g200762; PIDN:AAA40060.1; PID:g200763
R;Samuelson, L.C.; Wiebauer, K.; Howard, G.; Schmid, R.M.; Koeplin, D.; Meisler, M.H.
Nucleic Acids Res. 19, 6935-6941, 1991
A;Title: Isolation of the murine ribonuclease gene Rib-1: structure and tissue specific e
A;Reference number: S22598; MUID:92107684; PMID:1840677
A;Accession: S22598
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-149 <SAM>
A;Cross-references: EMBL:X60103; NID:g53981; PIDN:CAA42697.1; PID:g53982
R;Lenstra, J.A.; Beintema, J.J.
Eur. J. Biochem. 98, 399-408, 1979
A;Title: The amino acid sequence of mouse pancreatic ribonuclease.
A;Reference number: A00830; MUID:80024269; PMID:556267
A;Accession: A00830
A;Molecule type: protein
A;Residues: 26-149 <LEN>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-149/Product: pancreatic ribonuclease #status experimental <MAT>
F;37,66,144/Active site: His, Lys, His #status predicted
F;51-109,65-120,83-135,90-97/Disulfide bonds: #status predicted
F;62,87/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             19.3%;  Score 116.5;  DB 1;  Length 149;
  Best Local Similarity   29.9%;  Pred. No. 0.00018;
  Matches   35;  Conservative   17;  Mismatches   42;  Indels   23;  Gaps    7;
```

NRPG
pancreatic ribonuclease (EC 3.1.27.5) - pig
N;Alternate names: RNase 1; RNase A
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
C;Accession: A92071; A91391; A00816
R;Jackson, R.L.; Hirs, C.H.W.
J. Biol. Chem. 245, 637-653, 1970
A;Title: The primary structure of porcine pancreatic ribonuclease. II. The amino acid se
A;Reference number: A92071; MUID:70104197; PMID:5460946
A;Accession: A92071
A;Molecule type: protein
A;Residues: 1,'Q',3-124 <JAC>
R;Wierenga, R.K.; Huizinga, J.D.; Gaastra, W.; Welling, G.W.; Beintema, J.J.
FEBS Lett. 31, 181-185, 1973
A;Title: Affinity chromatography of porcine pancreatic ribonuclease and reinvestigation
A;Reference number: A91391
A;Accession: A91391
A;Molecule type: protein
A;Residues: 1-124 <WIE>
R;Phelan, J.J.; Hirs, C.H.W.
J. Biol. Chem. 245, 654-661, 1970
A;Title: The primary structure of porcine pancreatic ribonuclease. III. The disulfide bo
A;Reference number: A92072; MUID:70104198; PMID:4904878
A;Contents: annotation; disulfide bonds
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;21,34,76/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status experimental

Query Match 21.4%; Score 129.5; DB 1; Length 124;
Best Local Similarity 30.7%; Pred. No. 7.6e-06;
Matches 35; Conservative 20; Mismatches 42; Indels 17; Gaps 6;

```
Qy          7 FQQKHI------INTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGV-INLN 59
              ||::|:       |:   || ::     :  |:|| ||||:  |   |:|:|: : :|
Db          8 FQRQHMDPDSSSSNSSNYCNLMMSRR-NMTQGRCKPVNTFVHESLADVQAVCSQINVNCK 66

Qy         60 VLSTTRFQLNT------CTRTSITPRP-CPYSSRTETNYICVKCENQ--YPVHF 104
                 |  :| |:      | :|  :  | | | :  |  :| | ||     ||||
Db         67 NGQTNCYQSNSTMHITDCRQTGSSKYPNCAYKASQEQKHIIVACEGNPPVPVHF 120
```

RESULT 8
S20066
pancreatic-type ribonuclease (EC 3.1.27.5) BRb precursor, brain - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 22-Nov-1993 #sequence_revision 12-May-1995 #text_change 22-Jun-1999
C;Accession: S20066; JX0056
R;Sasso, M.P.; Carsana, A.; Confalone, E.; Cosi, C.; Sorrentino, S.; Viola, M.; Palmieri
Nucleic Acids Res. 19, 6469-6474, 1991
A;Title: Molecular cloning of the gene encoding the bovine brain ribonuclease and its ex
A;Reference number: S20066; MUID:92093604; PMID:1754384
A;Accession: S20066
A;Molecule type: DNA
A;Residues: 1-167 <SAS>
A;Cross-references: EMBL:X59767; NID:g150; PIDN:CAA42439.1; PID:g151
R;Watanabe, H.; Katoh, H.; Ishii, M.; Komoda, Y.; Sanda, A.; Takizawa, Y.; Ohgi, K.; Iri
J. Biochem. 104, 939-945, 1988
A;Title: Primary structure of a ribonuclease from bovine brain.
A;Reference number: JX0056; MUID:89214015; PMID:3243767
A;Accession: JX0056
A;Molecule type: protein
A;Residues: 27-154,'S',156-166 <WAT>
A;Experimental source: brain
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase
F;38,67,145/Active site: His, Lys, His #status predicted
F;52-110,66-121,84-136,91-98/Disulfide bonds: #status predicted
F;88/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;155/Binding site: carbohydrate (Thr) (covalent) #status experimental
F;159/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match 21.4%; Score 129.5; DB 2; Length 167;
Best Local Similarity 30.6%; Pred. No. 1e-05;
Matches 37; Conservative 18; Mismatches 43; Indels 23; Gaps 7;

```
Qy          5 ATFQQKHI------INTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINL 58
              | |:::|:       : |  || ::     :  |:|| ||||:  |   |||:|:
Db         32 AKFRRQHMDSGSSSSSNPNYCNQMMKRR-RMTHGRCKPVNTFVHESLDDVKAVCS---QK 87

Qy         59 NVL----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHFA 105
              |:           | :   :  |  |  :  | | | :  :  || | || | | ||||
Db         88 NITCKNGHPNCYQSKSTMSITDCRETGSSKYPNCAYKTSQKQKYITVACEGNPYVPVHFD 147

Qy        106 G 106
              |
Db        148 G 148
```

RESULT 9
S41111
pancreatic ribonuclease - common iguana
C;Species: Iguana iguana (common iguana)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Aug-1998
C;Accession: S41111
R;Zhao, W.; Beintema, J.J.; Hofsteenge, J.
Eur. J. Biochem. 219, 641-646, 1994
A;Title: The amino acid sequence of iguana (Iguana iguana) pancreatic ribonuclease.
A;Reference number: S41111; MUID:94139745; PMID:8307028
A;Accession: S41111
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-119 <ZHA>
C;Superfamily: pancreatic ribonuclease

Query Match 21.1%; Score 127.5; DB 2; Length 119;
Best Local Similarity 29.6%; Pred. No. 1.1e-05;
Matches 34; Conservative 17; Mismatches 51; Indels 13; Gaps 4;

```
Qy          2 QNWATFQQKHI-------INTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAIC-- 52
              |:|::|| |||         |    |: ::     :   :||  |||: :| : :: :|
Db          1 QDWSSFQNKHIDYPETSASNPNAYCDLMMQRR-NLNPTKCKTRNTFVHASPSEIQQVCGS 59

Qy         53 --TGVINLNVLSTTRFQLNTCTRTSIT-PRPCPYSSRTETNYICVKCENQYPVHF 104
                 |   :    |   | | |      | | | | |:    |  | : |||  ||||
Db         60 GGTHYEDNLYDSNESFDLTDCKNVGGTAPSSCKYNGTPGTKRIRIACENNQPVHF 114
```

RESULT 10
NRKGR
pancreatic ribonuclease (EC 3.1.27.5) - red kangaroo
N;Alternate names: RNase 1; RNase A
C;Species: Macropus rufus, Megaleia rufa (red kangaroo)
C;Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 04-Oct-1996
C;Accession: A00833
R;Gaastra, W.; Welling, G.W.; Beintema, J.J.
Eur. J. Biochem. 86, 209-217, 1978
A;Title: The amino-acid sequence of kangaroo pancreatic ribonuclease.
A;Reference number: A00833; MUID:78190621; PMID:658039
A;Accession: A00833
A;Molecule type: protein
A;Residues: 1-122 <GAA>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;11,40,117/Active site: His, Lys, His #status predicted
F;25-83,39-94,57-109,64-71/Disulfide bonds: #status predicted
F;61/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 19.7%; Score 119; DB 1; Length 122;
Best Local Similarity 29.8%; Pred. No. 8.2e-05;
Matches 34; Conservative 17; Mismatches 45; Indels 18; Gaps 6;

```
Qy          7 FQQKHI------INTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAIC-------- 52
              ||::|:       ::   || ::     :  |:|| :||||    : | |:|
```

```
Qy          2 QNWATFQQKHIINTP-IICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGV-INLN 59
              |||| ||:||| ||  | |||:| :|||||||||  ||||||||||||||:|   | |
Db          1 QNWAKFQEKHIPNTSNINCNTIMDKSIYIVGGQCKERNTFIISSATTVKAICSGASTNRN 60

Qy         60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              |||||||||||  |::  ||||||:|||||| |||||||: ||||||||||
Db         61 VLSTTRFQLNTCIRSATAPRPCPYNSRTETNVICVKCENRLPVHFAGIGRC 111


RESULT 3
JX0085
pancreatic ribonuclease (EC 3.1.27.5) - bullfrog
C;Species: Rana catesbeiana (bullfrog)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994
C;Accession: JX0085
R;Nitta, R.; Katayama, N.; Okabe, Y.; Iwama, M.; Watanabe, H.; Abe, Y.; Okazaki, T.; Ohg
J. Biochem. 106, 729-735, 1989
A;Title: Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver.
A;Reference number: JX0085; MUID:90130374; PMID:2613682
A;Accession: JX0085
A;Molecule type: protein
A;Residues: 1-111 <NIT>
C;Superfamily: pancreatic ribonuclease
C;Keywords: hydrolase; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10,35,104/Active site: His, Lys, His #status predicted
F;19-72,34-82,52-97,94-111/Disulfide bonds: #status predicted

  Query Match             61.2%;  Score 370;  DB 2;  Length 111;
  Best Local Similarity   64.9%;  Pred. No. 1e-29;
  Matches   72;  Conservative   10;  Mismatches   27;  Indels    2;  Gaps    2;

Qy          2 QNWATFQQKHIINTPII-CNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 59
              |||| |::||| :|  | ||||:|  ||||||:||  |||||||   |||||:||  :
Db          1 QNWAKFKEKHIRSTSSIDCNTIMDKAIYIVGGKCKERNTFIISSEDNVKAICSGVSPDRK 60

Qy         60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              |||| |:|||| | |||||||||    : | ||||||  | |||| |||:|
Db         61 ELSTTSFKLNTCIRDSITPRPCPYHPSPDNNKICVKCEKQLPVHFVGIGKC 111


RESULT 4
A39035
ribonuclease-related anti-tumor protein - northern leopard frog (fragment)
C;Species: Rana pipiens (northern leopard frog)
C;Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993
C;Accession: A39035
R;Ardelt, W.; Mikulski, S.M.; Shogen, K.
J. Biol. Chem. 266, 245-251, 1991
A;Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and earl
A;Reference number: A39035; MUID:91093131; PMID:1985896
A;Accession: A39035
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-104 <ARD>
C;Superfamily: pancreatic ribonuclease

  Query Match             44.7%;  Score 270.5;  DB 2;  Length 104;
  Best Local Similarity   47.7%;  Pred. No. 6.9e-20;
  Matches   53;  Conservative   17;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          2 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 59
              ::| |||:||| ||  : |: |:  |::     ||  |||| |    ||||| |:| : |
Db          1 EDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56

Qy         60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104


RESULT 5
A35932
angiogenin precursor - mouse
N;Alternate names: angiogenesis factor
N;Contains: ribonuclease (EC 3.1.27.-)
C;Species: Mus musculus (house mouse)
C;Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 18-Jun-1999
C;Accession: A35932
R;Bond, M.D.; Vallee, B.L.
Biochem. Biophys. Res. Commun. 171, 988-995, 1990
A;Title: Isolation and sequencing of mouse angiogenin DNA.
A;Reference number: A35932; MUID:91025023; PMID:2222458
A;Accession: A35932
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-145 <BON>
A;Cross-references: GB:U22516; NID:g726325; PIDN:AAA91366.1; PID:g726326
C;Genetics:
A;Introns: #status absent
C;Function:
A;Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues
C;Superfamily: pancreatic ribonuclease
C;Keywords: angiogenesis; hydrolase; nucleic acid degradation; pyroglutamic acid
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-145/Product: angiogenin #status predicted <MAT>
F;25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;37,64,137/Active site: His, Lys, His #status predicted
F;50-104,63-115,81-130/Disulfide bonds: #status predicted

  Query Match             22.6%;  Score 136.5;  DB 1;  Length 145;
  Best Local Similarity   40.3%;  Pred. No. 1.8e-06;
  Matches   31;  Conservative   11;  Mismatches   28;  Indels    7;  Gaps    3;

Qy         34 CKRVNTFIISSATTVKAICTG-----VINLNVLSTTRFQLNTCTRTSITPR-PCPYSSRT 87
              || |||||  : : :||||         ||  :| : ||: ||  |  :|| || | :
Db         63 CKDVNTFIHGNKSNIKAICGANGSPYRENLR-MSKSPFQVTTCKHTGGSPRPPCQYRASA 121

Qy         88 ETNYICVKCENQYPVHF 104
                 :: : |||  ||||
Db        122 GFRHVVIACENGLPVHF 138


RESULT 6
NRWHK
pancreatic ribonuclease (EC 3.1.27.5) - minke whale
N;Alternate names: RNase 1; RNase A
C;Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
C;Accession: A00818
R;Emmens, M.; Welling, G.W.; Beintema, J.J.
Biochem. J. 157, 317-323, 1976
A;Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclease.
A;Reference number: A00818; MUID:76277855; PMID:962870
A;Accession: A00818
A;Molecule type: protein
A;Residues: 1-124 <EMM>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F;76/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

  Query Match             21.7%;  Score 131.5;  DB 1;  Length 124;
  Best Local Similarity   32.5%;  Pred. No. 4.8e-06;
  Matches   38;  Conservative   17;  Mismatches   39;  Indels   23;  Gaps    7;

Qy          7 FQQKHII------NTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 60
              ||::|:       | |  || ::     :  |:|| ||||:  |   |||:|:     ||
Db          8 FQRQHMDSGNSPGNNPNYCNQMMMRR-KMTQGRCKPVNTFVHESLEDVKAVCS---QKNV 63

Qy         61 L----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 104
              |          | :   :  | :|  :  | | | :  :  :| | || | | ||||
Db         64 LCKNGRTNCYESNSTMHITDCRQTGSSKYPNCAYKTSQKEKHIIVACEGNPYVPVHF 120


RESULT 7
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 7, 2004, 21:38:36 ; Search time 10.072 Seconds
(without alignments)
1060.090 Million cell updates/sec

Title: US-09-961-400-21
Perfect score: 605
Sequence: 1 MQNWATFQQKHIINTPIICN.....ICVKCENQYPVHFAGIGRCP 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	582.5	96.3	111	2	A27121	ribonuclease-relat
2	451	74.5	111	1	JX0120	ribonuclease-relat
3	370	61.2	111	2	JX0085	pancreatic ribonuc
4	270.5	44.7	104	2	A39035	ribonuclease-relat
5	136.5	22.6	145	1	A35932	angiogenin precurs
6	131.5	21.7	124	1	NRWHK	pancreatic ribonuc
7	129.5	21.4	124	1	NRPG	pancreatic ribonuc
8	129.5	21.4	167	2	S20066	pancreatic-type ri
9	127.5	21.1	119	2	S41111	pancreatic ribonuc
10	119	19.7	122	1	NRKGR	pancreatic ribonuc
11	118.5	19.6	123	1	A43825	angiogenin - pig
12	118.5	19.6	124	1	NRPRH	pancreatic ribonuc
13	116.5	19.3	128	1	NRCU	pancreatic ribonuc
14	116.5	19.3	149	1	NRMS	pancreatic ribonuc
15	114.5	18.9	128	1	NRGPB	pancreatic ribonuc
16	114	18.8	125	1	A32474	angiogenin [valida
17	113.5	18.8	124	1	NRCM	pancreatic ribonuc
18	113.5	18.8	124	1	NRCMM	pancreatic ribonuc
19	113.5	18.8	124	1	NRCMB	pancreatic ribonuc
20	113.5	18.8	128	1	NRHO	pancreatic ribonuc
21	113	18.7	147	1	NRHUAG	angiogenin precurs
22	112.5	18.6	128	1	NRKS	pancreatic ribonuc
23	110.5	18.3	124	2	S08549	ribonuclease - dom
24	109.5	18.1	124	1	NRDEN	pancreatic ribonuc
25	109	18.0	125	1	B43825	angiogenin - rabbi
26	108.5	17.9	124	1	NRGF	pancreatic ribonuc
27	108.5	17.9	124	1	NRDEO	pancreatic ribonuc
28	108.5	17.9	130	2	S22808	pancreatic ribonuc
29	107.5	17.8	124	1	NRWB	pancreatic ribonuc
30	107.5	17.8	158	2	I61900	eosinophil-derived
31	106.5	17.6	124	1	NRBOB	pancreatic ribonuc
32	106.5	17.6	124	1	NREKN	pancreatic ribonuc
33	106.5	17.6	124	2	S07141	pancreatic ribonuc
34	106.5	17.6	150	1	NRBO	pancreatic ribonuc
35	105.5	17.4	119	2	JX0115	pancreatic ribonuc
36	105.5	17.4	124	1	NRSH	pancreatic ribonuc
37	105.5	17.4	152	1	NRRT	pancreatic ribonuc
38	104.5	17.3	124	1	NRCB	pancreatic ribonuc
39	103.5	17.1	125	4	A47498	seminal ribonuclea
40	103.5	17.1	150	1	NRBOS	seminal ribonuclea
41	102.5	16.9	124	1	NRHP	pancreatic ribonuc
42	101	16.7	125	2	S04503	pancreatic ribonuc
43	100.5	16.6	124	1	NRGN	pancreatic ribonuc
44	100.5	16.6	124	1	NRDEF	pancreatic ribonuc
45	100.5	16.6	124	2	S08546	pancreatic ribonuc

ALIGNMENTS

RESULT 1
A27121
ribonuclease-related sialic acid-binding lectin - bullfrog
C;Species: Rana catesbeiana (bullfrog)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 30-Jun-1993
C;Accession: A27121
R;Titani, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kawauchi, H.; Takayanag
Biochemistry 26, 2189-2194, 1987
A;Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana)
A;Reference number: A27121; MUID:87299649; PMID:3304421
A;Accession: A27121
A;Molecule type: protein
A;Residues: 1-111 <TIT>
C;Superfamily: pancreatic ribonuclease
C;Keywords: lectin

Query Match 96.3%; Score 582.5; DB 2; Length 111;
Best Local Similarity 96.4%; Pred. No. 9.5e-51;
Matches 107; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

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Qy          2 QNWATFQQKHIINTPII-CNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 60
              :|||||||||||||||| ||||:|||||||||||||||||||||||||||||:||
Db          1 ENWATFQQKHIINTPIINCNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60

Qy         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
```

RESULT 2
JX0120
ribonuclease-related sialic acid-binding lectin - Japanese frog
C;Species: Rana japonica (Japanese frog)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JX0120
R;Kamiya, Y.; Oyama, F.; Oyama, R.; Sakakibara, F.; Nitta, K.; Kawauchi, H.; Takayanagi
J. Biochem. 108, 139-143, 1990
A;Title: Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs.
A;Reference number: JX0120; MUID:91035319; PMID:2229005
A;Accession: JX0120
A;Molecule type: protein
A;Residues: 1-111 <KAM>
A;Experimental source: egg
C;Superfamily: pancreatic ribonuclease
C;Keywords: lectin; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;19-72,34-82,52-97,94-111/Disulfide bonds: #status experimental

Query Match 74.5%; Score 451; DB 1; Length 111;
Best Local Similarity 77.5%; Pred. No. 1e-37;
Matches 86; Conservative 8; Mismatches 15; Indels 2; Gaps 2;

```
;   ORGANISM: Rana pipiens
US-09-961-400-9

  Query Match             47.0%;  Score 284.5;  DB 10;  Length 111;
  Best Local Similarity   50.0%;  Pred. No. 1.9e-24;
  Matches   56;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          1 MQNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NL 58
              ||:| |||:||: ||  : || ||  |::     ||  |||| |    ||||| |:| :
Db          7 MQDWLTFQKKHLTNTRDVDCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASK 62

Qy         59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              |||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         63 NVLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 111


Search completed: May  7, 2004, 21:51:59
Job time : 36.6155 secs
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;  APPLICANT:  Department of Health and Human Services
;  TITLE OF INVENTION: Recombinant Anti-Tumor RNase
;  FILE REFERENCE: 015280-343110US
;  CURRENT APPLICATION NUMBER: US/09/948,391A
;  CURRENT FILING DATE:  2002-05-10
;  PRIOR APPLICATION NUMBER: US 60/079,751
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: WO PCT/US99/06641
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: US 09/622,613
;  PRIOR FILING DATE: 2000-08-17
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Rana
;   OTHER INFORMATION: catesbeiana ribonuclease with Met22Leu and
;   OTHER INFORMATION: Met57Leu substitutions (recombinant RaCOR1
;   OTHER INFORMATION: Met22Leu Met57Leu)
US-09-948-391A-19

  Query Match             98.2%;  Score 594;  DB 10;  Length 110;
  Best Local Similarity   99.1%;  Pred. No. 1.3e-59;
  Matches  109;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 QNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 61
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QNWATFQQKHIIKTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 60

Qy         62 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110


RESULT 13
US-09-948-391A-24
; Sequence 24, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
;  APPLICANT: Rybak, Susanna M.
;  APPLICANT:  Newton, Dianne L.
;  APPLICANT:  The United States of America
;  APPLICANT:  as represented by The Secretary of the
;  APPLICANT:  Department of Health and Human Services
;  TITLE OF INVENTION: Recombinant Anti-Tumor RNase
;  FILE REFERENCE: 015280-343110US
;  CURRENT APPLICATION NUMBER: US/09/948,391A
;  CURRENT FILING DATE:  2002-05-10
;  PRIOR APPLICATION NUMBER: US 60/079,751
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: WO PCT/US99/06641
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: US 09/622,613
;  PRIOR FILING DATE: 2000-08-17
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Rana
;   OTHER INFORMATION: catesbeiana ribonuclease with Gln1Ser substitution
;   OTHER INFORMATION: (recombinant RaCOR1 Q1S)
US-09-948-391A-24

  Query Match             97.7%;  Score 591;  DB 10;  Length 110;
  Best Local Similarity   98.2%;  Pred. No. 2.9e-59;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 NWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVLS 62
              |||||||||||||||||||:|||||||||||||||||||||||||||||||||||:||||
Db          2 NWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS 61

Qy         63 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110


RESULT 14
US-09-961-400-24
; Sequence 24, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
;  APPLICANT: RYBAK, SUSANNA M.
;  APPLICANT:  GOLDENBERG, DAVID M.
;  APPLICANT:  NEWTON, DIANNE L.
;  TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
;  TITLE OF INVENTION:  CELLS
;  FILE REFERENCE: 018733/1059
;  CURRENT APPLICATION NUMBER: US/09/961,400
;  CURRENT FILING DATE:  2001-09-25
;  PRIOR APPLICATION NUMBER: 09/622,613
;  PRIOR FILING DATE: 2000-08-17
;  PRIOR APPLICATION NUMBER: PCT/US99/06641
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: 60/079,751
;  PRIOR FILING DATE: 1998-03-26
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: Rana catesbeiana
US-09-961-400-24

  Query Match             97.7%;  Score 591;  DB 10;  Length 110;
  Best Local Similarity   98.2%;  Pred. No. 2.9e-59;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 NWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVLS 62
              |||||||||||||||||||:|||||||||||||||||||||||||||||||||||:||||
Db          2 NWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS 61

Qy         63 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110


RESULT 15
US-09-961-400-9
; Sequence 9, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
;  APPLICANT: RYBAK, SUSANNA M.
;  APPLICANT:  GOLDENBERG, DAVID M.
;  APPLICANT:  NEWTON, DIANNE L.
;  TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
;  TITLE OF INVENTION:  CELLS
;  FILE REFERENCE: 018733/1059
;  CURRENT APPLICATION NUMBER: US/09/961,400
;  CURRENT FILING DATE:  2001-09-25
;  PRIOR APPLICATION NUMBER: 09/622,613
;  PRIOR FILING DATE: 2000-08-17
;  PRIOR APPLICATION NUMBER: PCT/US99/06641
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: 60/079,751
;  PRIOR FILING DATE: 1998-03-26
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 111
;   TYPE: PRT
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Db          1 QNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 60

Qy         62 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110


RESULT 9
US-09-948-391A-26
; Sequence 26, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
;  APPLICANT: Rybak, Susanna M.
;  APPLICANT:  Newton, Dianne L.
;  APPLICANT:  The United States of America
;  APPLICANT:  as represented by The Secretary of the
;  APPLICANT:  Department of Health and Human Services
;  TITLE OF INVENTION: Recombinant Anti-Tumor RNase
;  FILE REFERENCE: 015280-343110US
;  CURRENT APPLICATION NUMBER: US/09/948,391A
;  CURRENT FILING DATE:  2002-05-10
;  PRIOR APPLICATION NUMBER: US 60/079,751
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: WO PCT/US99/06641
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: US 09/622,613
;  PRIOR FILING DATE: 2000-08-17
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
;   LENGTH: 111
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Rana
;   OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1
;   OTHER INFORMATION: and Gln2Ser substitution (Met(-1) RaCOR1 Q1S)
US-09-948-391A-26

  Query Match             98.5%;  Score 596;  DB 10;  Length 111;
  Best Local Similarity   97.3%;  Pred. No. 7.9e-60;
  Matches  108;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MQNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 60
              | |||||||||||||||||||:||||||||||||||||||||||||||||||:||
Db          1 MSNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60

Qy         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111


RESULT 10
US-09-961-400-26
; Sequence 26, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
;  APPLICANT: RYBAK, SUSANNA M.
;  APPLICANT:  GOLDENBERG, DAVID M.
;  APPLICANT:  NEWTON, DIANNE L.
;  TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
;  TITLE OF INVENTION:  CELLS
;  FILE REFERENCE: 018733/1059
;  CURRENT APPLICATION NUMBER: US/09/961,400
;  CURRENT FILING DATE:  2001-09-25
;  PRIOR APPLICATION NUMBER: 09/622,613
;  PRIOR FILING DATE: 2000-08-17
;  PRIOR APPLICATION NUMBER: PCT/US99/06641
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: 60/079,751
;  PRIOR FILING DATE: 1998-03-26
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
;   LENGTH: 111
;   TYPE: PRT
;   ORGANISM: Rana catesbeiana
US-09-961-400-26

  Query Match             98.5%;  Score 596;  DB 10;  Length 111;
  Best Local Similarity   97.3%;  Pred. No. 7.9e-60;
  Matches  108;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MQNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 60
              | |||||||||||||||||||:||||||||||||||||||||||||||||||:||
Db          1 MSNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60

Qy         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111


RESULT 11
US-09-948-391A-17
; Sequence 17, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
;  APPLICANT: Rybak, Susanna M.
;  APPLICANT:  Newton, Dianne L.
;  APPLICANT:  The United States of America
;  APPLICANT:  as represented by The Secretary of the
;  APPLICANT:  Department of Health and Human Services
;  TITLE OF INVENTION: Recombinant Anti-Tumor RNase
;  FILE REFERENCE: 015280-343110US
;  CURRENT APPLICATION NUMBER: US/09/948,391A
;  CURRENT FILING DATE:  2002-05-10
;  PRIOR APPLICATION NUMBER: US 60/079,751
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: WO PCT/US99/06641
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: US 09/622,613
;  PRIOR FILING DATE: 2000-08-17
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
;   LENGTH: 111
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Rana
;   OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1
;   OTHER INFORMATION: (recombinant Met(-1) RaCOR1)
US-09-948-391A-17

  Query Match             98.3%;  Score 595;  DB 10;  Length 111;
  Best Local Similarity   97.3%;  Pred. No. 1e-59;
  Matches  108;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MQNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 60
              |||||||||||||||||||:||||||||||||||||||||||||||||||:||
Db          1 MQNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVTTFIISSATTVKAICTGVINMNV 60

Qy         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111


RESULT 12
US-09-948-391A-19
; Sequence 19, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
;  APPLICANT: Rybak, Susanna M.
;  APPLICANT:  Newton, Dianne L.
;  APPLICANT:  The United States of America
;  APPLICANT:  as represented by The Secretary of the
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;  CURRENT FILING DATE:  2001-09-25
;  PRIOR APPLICATION NUMBER: 09/622,613
;  PRIOR FILING DATE: 2000-08-17
;  PRIOR APPLICATION NUMBER: PCT/US99/06641
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: 60/079,751
;  PRIOR FILING DATE: 1998-03-26
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
;   LENGTH: 111
;   TYPE: PRT
;   ORGANISM: Rana catesbeiana
US-09-961-400-17

  Query Match             99.3%;  Score 601;  DB 10;  Length 111;
  Best Local Similarity   98.2%;  Pred. No. 2.1e-60;
  Matches  109;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MQNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 60
              |||||||||||||||||||||||:|||||||||||||||||||||||||||||||:||
Db          1 MQNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60

Qy         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111


RESULT 6
US-09-961-400-19
; Sequence 19, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
;  APPLICANT: RYBAK, SUSANNA M.
;  APPLICANT:  GOLDENBERG, DAVID M.
;  APPLICANT:  NEWTON, DIANNE L.
;  TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
;  TITLE OF INVENTION:  CELLS
;  FILE REFERENCE: 018733/1059
;  CURRENT APPLICATION NUMBER: US/09/961,400
;  CURRENT FILING DATE:  2001-09-25
;  PRIOR APPLICATION NUMBER: 09/622,613
;  PRIOR FILING DATE: 2000-08-17
;  PRIOR APPLICATION NUMBER: PCT/US99/06641
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: 60/079,751
;  PRIOR FILING DATE: 1998-03-26
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: Rana catesbeiana
US-09-961-400-19

  Query Match             99.2%;  Score 600;  DB 10;  Length 110;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-60;
  Matches  110;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 QNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 60

Qy         62 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110


RESULT 7
US-09-948-391A-15
; Sequence 15, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
;  APPLICANT: Rybak, Susanna M.
;  APPLICANT:  Newton, Dianne L.
;  APPLICANT:  The United States of America
;  APPLICANT:  as represented by The Secretary of the
;  APPLICANT:  Department of Health and Human Services
;  TITLE OF INVENTION: Recombinant Anti-Tumor RNase
;  FILE REFERENCE: 015280-343110US
;  CURRENT APPLICATION NUMBER: US/09/948,391A
;  CURRENT FILING DATE:  2002-05-10
;  PRIOR APPLICATION NUMBER: US 60/079,751
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: WO PCT/US99/06641
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: US 09/622,613
;  PRIOR FILING DATE: 2000-08-17
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Rana
;   OTHER INFORMATION: catesbeiana oocyte ribonuclease (RaCOR1) synthetic
;   OTHER INFORMATION: gene modified to use E. coli preferred codons
US-09-948-391A-15

  Query Match             98.5%;  Score 596;  DB 10;  Length 110;
  Best Local Similarity   98.2%;  Pred. No. 7.8e-60;
  Matches  108;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 QNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 61
              ||||||||||||||||||||||:|||||||||||||||||||||||||||||||:|||
Db          1 QNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 60

Qy         62 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110


RESULT 8
US-09-961-400-15
; Sequence 15, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
;  APPLICANT: RYBAK, SUSANNA M.
;  APPLICANT:  GOLDENBERG, DAVID M.
;  APPLICANT:  NEWTON, DIANNE L.
;  TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
;  TITLE OF INVENTION:  CELLS
;  FILE REFERENCE: 018733/1059
;  CURRENT APPLICATION NUMBER: US/09/961,400
;  CURRENT FILING DATE:  2001-09-25
;  PRIOR APPLICATION NUMBER: 09/622,613
;  PRIOR FILING DATE: 2000-08-17
;  PRIOR APPLICATION NUMBER: PCT/US99/06641
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: 60/079,751
;  PRIOR FILING DATE: 1998-03-26
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: Rana catesbeiana
US-09-961-400-15

  Query Match             98.5%;  Score 596;  DB 10;  Length 110;
  Best Local Similarity   98.2%;  Pred. No. 7.8e-60;
  Matches  108;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 QNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 61
              ||||||||||||||||||||||:|||||||||||||||||||||||||||||||:|||
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                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MQNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 60

Qy         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111


RESULT 2
US-09-961-400-21
; Sequence 21, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
;  APPLICANT: RYBAK, SUSANNA M.
;  APPLICANT:  GOLDENBERG, DAVID M.
;  APPLICANT:  NEWTON, DIANNE L.
;  TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
;  TITLE OF INVENTION:  CELLS
;  FILE REFERENCE: 018733/1059
;  CURRENT APPLICATION NUMBER: US/09/961,400
;  CURRENT FILING DATE:  2001-09-25
;  PRIOR APPLICATION NUMBER: 09/622,613
;  PRIOR FILING DATE: 2000-08-17
;  PRIOR APPLICATION NUMBER: PCT/US99/06641
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: 60/079,751
;  PRIOR FILING DATE: 1998-03-26
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
;   LENGTH: 111
;   TYPE: PRT
;   ORGANISM: Rana catesbeiana
US-09-961-400-21

  Query Match            100.0%;  Score 605;  DB 10;  Length 111;
  Best Local Similarity  100.0%;  Pred. No. 7.5e-61;
  Matches  111;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MQNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MQNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 60

Qy         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111


RESULT 3
US-09-948-391A-22
; Sequence 22, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
;  APPLICANT: Rybak, Susanna M.
;  APPLICANT:  Newton, Dianne L.
;  APPLICANT:  The United States of America
;  APPLICANT:  as represented by The Secretary of the
;  APPLICANT:  Department of Health and Human Services
;  TITLE OF INVENTION: Recombinant Anti-Tumor RNase
;  FILE REFERENCE: 015280-343110US
;  CURRENT APPLICATION NUMBER: US/09/948,391A
;  CURRENT FILING DATE:  2002-05-10
;  PRIOR APPLICATION NUMBER: US 60/079,751
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: WO PCT/US99/06641
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: US 09/622,613
;  PRIOR FILING DATE: 2000-08-17
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Rana
;   OTHER INFORMATION: catesbeiana ribonuclease with (His)6 tag, Met at
;   OTHER INFORMATION: position 7, Met23Leu and Met58Leu substitutions
;   OTHER INFORMATION: (recombinant Met(-1) RaCOR1 Met22Leu Met57Leu-(His)6)
US-09-948-391A-22

  Query Match            100.0%;  Score 605;  DB 10;  Length 117;
  Best Local Similarity  100.0%;  Pred. No. 8e-61;
  Matches  111;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MQNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7 MQNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 66

Qy         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 117


RESULT 4
US-09-961-400-22
; Sequence 22, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
;  APPLICANT: RYBAK, SUSANNA M.
;  APPLICANT:  GOLDENBERG, DAVID M.
;  APPLICANT:  NEWTON, DIANNE L.
;  TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
;  TITLE OF INVENTION:  CELLS
;  FILE REFERENCE: 018733/1059
;  CURRENT APPLICATION NUMBER: US/09/961,400
;  CURRENT FILING DATE:  2001-09-25
;  PRIOR APPLICATION NUMBER: 09/622,613
;  PRIOR FILING DATE: 2000-08-17
;  PRIOR APPLICATION NUMBER: PCT/US99/06641
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: 60/079,751
;  PRIOR FILING DATE: 1998-03-26
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: Rana catesbeiana
US-09-961-400-22

  Query Match            100.0%;  Score 605;  DB 10;  Length 117;
  Best Local Similarity  100.0%;  Pred. No. 8e-61;
  Matches  111;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MQNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7 MQNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 66

Qy         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 117


RESULT 5
US-09-961-400-17
; Sequence 17, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
;  APPLICANT: RYBAK, SUSANNA M.
;  APPLICANT:  GOLDENBERG, DAVID M.
;  APPLICANT:  NEWTON, DIANNE L.
;  TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
;  TITLE OF INVENTION:  CELLS
;  FILE REFERENCE: 018733/1059
;  CURRENT APPLICATION NUMBER: US/09/961,400
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:40 ; Search time 35.6155 Seconds
(without alignments)
865.070 Million cell updates/sec

Title: US-09-961-400-21
Perfect score: 605
Sequence: 1 MQNWATFQQKHIINTPIICN.....ICVKCENQYPVHFAGIGRCP 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1140673 seqs, 277566755 residues

Total number of hits satisfying chosen parameters: 1140673

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	605	100.0	111	10	US-09-948-391A-21	Sequence 21, Appl
2	605	100.0	111	10	US-09-961-400-21	Sequence 21, Appl
3	605	100.0	117	10	US-09-948-391A-22	Sequence 22, Appl
4	605	100.0	117	10	US-09-961-400-22	Sequence 22, Appl
5	601	99.3	111	10	US-09-961-400-17	Sequence 17, Appl
6	600	99.2	110	10	US-09-961-400-19	Sequence 19, Appl
7	596	98.5	110	10	US-09-948-391A-15	Sequence 15, Appl
8	596	98.5	110	10	US-09-961-400-15	Sequence 15, Appl
9	596	98.5	111	10	US-09-948-391A-26	Sequence 26, Appl
10	596	98.5	111	10	US-09-961-400-26	Sequence 26, Appl
11	595	98.3	111	10	US-09-948-391A-17	Sequence 17, Appl
12	594	98.2	110	10	US-09-948-391A-19	Sequence 19, Appl
13	591	97.7	110	10	US-09-948-391A-24	Sequence 24, Appl
14	591	97.7	110	10	US-09-961-400-24	Sequence 24, Appl
15	284.5	47.0	111	10	US-09-961-400-9	Sequence 9, Appli
16	282.5	46.7	105	10	US-09-948-391A-6	Sequence 6, Appli
17	282.5	46.7	105	10	US-09-961-400-6	Sequence 6, Appli
18	281.5	46.5	105	10	US-09-961-400-8	Sequence 8, Appli
19	278.5	46.0	105	14	US-10-153-882-2	Sequence 2, Appli
20	277.5	45.9	104	10	US-09-961-400-2	Sequence 2, Appli
21	277.5	45.9	105	10	US-09-948-391A-13	Sequence 13, Appl
22	277.5	45.9	105	10	US-09-961-400-13	Sequence 13, Appl
23	277.5	45.9	127	10	US-09-948-391A-28	Sequence 28, Appl
24	277.5	45.9	127	10	US-09-961-400-28	Sequence 28, Appl
25	276.5	45.7	104	10	US-09-948-391A-2	Sequence 2, Appli
26	276.5	45.7	104	10	US-09-948-391A-4	Sequence 4, Appli
27	276.5	45.7	104	10	US-09-961-400-4	Sequence 4, Appli
28	272.5	45.0	104	10	US-09-948-391A-11	Sequence 11, Appl
29	272.5	45.0	104	10	US-09-961-400-11	Sequence 11, Appl
30	272.5	45.0	105	10	US-09-948-391A-8	Sequence 8, Appli
31	272.5	45.0	111	10	US-09-948-391A-9	Sequence 9, Appli
32	268.5	44.4	104	9	US-09-986-119-1	Sequence 1, Appli
33	268.5	44.4	104	10	US-09-918-887-1	Sequence 1, Appli
34	265.5	43.9	104	12	US-10-461-713-53	Sequence 53, Appl
35	202	33.4	83	9	US-09-986-119-3	Sequence 3, Appli
36	202	33.4	83	10	US-09-918-887-3	Sequence 3, Appli
37	161	26.6	169	13	US-10-016-447-2	Sequence 2, Appli
38	131.5	21.7	124	12	US-10-037-417-103	Sequence 103, App
39	127.5	21.1	119	12	US-10-016-248-89	Sequence 89, Appl
40	127.5	21.1	119	15	US-10-074-978A-139	Sequence 139, App
41	118	19.5	99	15	US-10-074-978A-141	Sequence 141, App
42	117	19.3	147	9	US-09-731-872-254	Sequence 254, App
43	117	19.3	147	10	US-09-876-997-254	Sequence 254, App
44	114	18.8	123	12	US-10-461-713-58	Sequence 58, Appl
45	114	18.8	124	13	US-10-016-447-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-948-391A-21
; Sequence 21, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1,
; OTHER INFORMATION: Met23Leu and Met58Leu substitutions (recombinant
; OTHER INFORMATION: Met(-1) RaCOR1 Met22Leu Met57Leu)
US-09-948-391A-21

Query Match 100.0%; Score 605; DB 10; Length 111;
Best Local Similarity 100.0%; Pred. No. 7.5e-61;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 60

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;    APPLICANT:  Wlodawer, Alexander
;    TITLE OF INVENTION:  Recombinant Ribonuclease Proteins
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/875,811
;      FILING DATE:  19-FEB-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/02588
;      FILING DATE:  19-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/011,800
;      FILING DATE:  21-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Faris, Susan K.
;      REGISTRATION NUMBER:  41,739
;      REFERENCE/DOCKET NUMBER:  015280-244100US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  59:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  251 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-875-811-59

  Query Match             45.2%;  Score 273.5;  DB 3;  Length 251;
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  Matches   54;  Conservative   16;  Mismatches   33;  Indels    9;  Gaps    4;

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Db        147 MSDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASK 202

Qy         59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              |||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
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Search completed: May  7, 2004, 21:40:46
Job time : 12.8756 secs
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;    MOLECULE TYPE:  protein
US-09-095-429-1

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  Best Local Similarity   48.6%;  Pred. No. 2.8e-24;
  Matches   54;  Conservative   16;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          2 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 59
              |:| |||:||| ||  : |: |:  |::     ||  |||| |    ||||| |:| : |
Db          1 QDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56

Qy         60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104


RESULT 13
US-08-875-811-32
; Sequence 32, Application US/08875811
; Patent No. 6045793
;  GENERAL INFORMATION:
;    APPLICANT:  Rybak, Susanna M.
;    APPLICANT:  Newton, Dianne L.
;    APPLICANT:  Boque, Lluis
;    APPLICANT:  Wlodawer, Alexander
;    TITLE OF INVENTION:  Recombinant Ribonuclease Proteins
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/875,811
;      FILING DATE:  19-FEB-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/02588
;      FILING DATE:  19-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/011,800
;      FILING DATE:  21-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Faris, Susan K.
;      REGISTRATION NUMBER:  41,739
;      REFERENCE/DOCKET NUMBER:  015280-244100US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  32:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  112 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-875-811-32

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  Best Local Similarity   48.2%;  Pred. No. 3.1e-24;
  Matches   54;  Conservative   16;  Mismatches   33;  Indels    9;  Gaps    4;

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Qy         59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              |||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         64 NVLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 112


RESULT 14
US-08-875-811-63
; Sequence 63, Application US/08875811
; Patent No. 6045793
;  GENERAL INFORMATION:
;    APPLICANT:  Rybak, Susanna M.
;    APPLICANT:  Newton, Dianne L.
;    APPLICANT:  Boque, Lluis
;    APPLICANT:  Wlodawer, Alexander
;    TITLE OF INVENTION:  Recombinant Ribonuclease Proteins
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/875,811
;      FILING DATE:  19-FEB-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/02588
;      FILING DATE:  19-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/011,800
;      FILING DATE:  21-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Faris, Susan K.
;      REGISTRATION NUMBER:  41,739
;      REFERENCE/DOCKET NUMBER:  015280-244100US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  63:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  129 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-875-811-63

  Query Match             45.2%;  Score 273.5;  DB 3;  Length 129;
  Best Local Similarity   48.6%;  Pred. No. 3.7e-24;
  Matches   54;  Conservative   16;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          2 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 59
              |:| |||:||| ||  : |: |:  |::     ||  |||| |    ||||| |:| : |
Db         26 QDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 81

Qy         60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         82 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 129


RESULT 15
US-08-875-811-59
; Sequence 59, Application US/08875811
; Patent No. 6045793
;  GENERAL INFORMATION:
;    APPLICANT:  Rybak, Susanna M.
;    APPLICANT:  Newton, Dianne L.
;    APPLICANT:  Boque, Lluis
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Db          1 QDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56

Qy         60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104


RESULT 10
US-09-687-748-2
; Sequence 2, Application US/09687748
; Patent No. 6423515
; GENERAL INFORMATION:
;  APPLICANT:  Saxena, Shailendra K
;  TITLE OF INVENTION:  METHODS OF MAKING NUCLEIC ACIDS ENCODING RIBONUCLEASES
;  FILE REFERENCE:  5013 US 01
;  CURRENT APPLICATION NUMBER: US/09/687,748
;  CURRENT FILING DATE:  2000-10-14
;  PRIOR APPLICATION NUMBER:  09/394,268
;  PRIOR FILING DATE:  1999-09-10
;  NUMBER OF SEQ ID NOS:  8
;  SOFTWARE:  PatentIn Ver. 2.0
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;   LENGTH: 104
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: SEQ ID NO:1 with Leu at position 23 and Cys at
;   OTHER INFORMATION: position 72
US-09-687-748-2

  Query Match             45.2%;  Score 273.5;  DB 4;  Length 104;
  Best Local Similarity   49.5%;  Pred. No. 2.8e-24;
  Matches   55;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          2 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 59
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Db          1 QDWLTFQKKHITNTRDVDCDNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56

Qy         60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         57 VLTTSEFYLSDC---NVTCRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104


RESULT 11
US-08-626-288-1
; Sequence 1, Application US/08626288
; Patent No. 6649392
;  GENERAL INFORMATION:
;    APPLICANT:  Youle, Richard
;    APPLICANT:  Vasandani, Veena
;    APPLICANT:  Wu, Yon-Neng
;    APPLICANT:  Boix, Ester
;    APPLICANT:  Ardelt, Wojeiech
;    TITLE OF INVENTION:  A Mutant Form of Cytotoxic Protein Which
;    TITLE OF INVENTION:  Allows Production by Recombinant Methods
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew
;      STREET:  One Market Plaza, Steuart Street Tower
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105-1492
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/626,288
;      FILING DATE:  No. 6649392 yet assigned
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ran, David B.
;      REGISTRATION NUMBER:  38,589
;      REFERENCE/DOCKET NUMBER:  15280-267
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 543-9600
;      TELEFAX:  (415) 543-5043
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  104 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-626-288-1

  Query Match             45.2%;  Score 273.5;  DB 4;  Length 104;
  Best Local Similarity   48.6%;  Pred. No. 2.8e-24;
  Matches   54;  Conservative   16;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          2 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 59
              |:| |||:||| ||  : |: |:  |::     ||  |||| |    |||| |:| : |
Db          1 QDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56

Qy         60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104


RESULT 12
US-09-095-429-1
; Sequence 1, Application US/09095429
; Patent No. 6649393
;  GENERAL INFORMATION:
;    APPLICANT:  Youle, Richard
;    APPLICANT:  Vasandani, Veena
;    APPLICANT:  Wu, Yon-Neng
;    APPLICANT:  Boix, Ester
;    APPLICANT:  Ardelt, Wojeiech
;    TITLE OF INVENTION:  A Mutant Form of Cytotoxic Protein Which
;    TITLE OF INVENTION:  Allows Production by Recombinant Methods
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew
;      STREET:  One Market Plaza, Steuart Street Tower
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105-1492
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/095,429
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/626,288
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ran, David B.
;      REGISTRATION NUMBER:  38,589
;      REFERENCE/DOCKET NUMBER:  15280-267
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 543-9600
;      TELEFAX:  (415) 543-5043
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  104 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
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;    APPLICANT:  Wlodawer, Alexander
;    TITLE OF INVENTION:  Recombinant Ribonuclease Proteins
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/875,811
;      FILING DATE:  19-FEB-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/02588
;      FILING DATE:  19-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/011,800
;      FILING DATE:  21-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Faris, Susan K.
;      REGISTRATION NUMBER:  41,739
;      REFERENCE/DOCKET NUMBER:  015280-244100US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  51:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  358 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-875-811-51

  Query Match             45.5%;  Score 275.5;  DB 3;  Length 358;
  Best Local Similarity   48.2%;  Pred. No. 7.5e-24;
  Matches   54;  Conservative   17;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          1 MQNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NL 58
              |::| |||:||| ||  : |: |:  |::     ||  |||| |    ||||| |:| : 
Db          1 MEDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASK 56

Qy         59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              |||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         57 NVLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 105


RESULT 7
US-09-394-268-1
; Sequence 1, Application US/09394268
; Patent No. 6175003
; GENERAL INFORMATION:
;  APPLICANT: Saxena, Shailendra K
;  TITLE OF INVENTION: NUCLEIC ACIDS ENCODING RIBONUCLEASES AND METHODS OF
;  TITLE OF INVENTION: MAKING THEM
;  FILE REFERENCE: 5013
;  CURRENT APPLICATION NUMBER: US/09/394,268
;  CURRENT FILING DATE: 1999-09-10
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 104
;   TYPE: PRT
;   ORGANISM: Rana pipiens
US-09-394-268-1

  Query Match             45.2%;  Score 273.5;  DB 3;  Length 104;
  Best Local Similarity   48.6%;  Pred. No. 2.8e-24;
  Matches   54;  Conservative   16;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          2 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 59
              |:| |||:||| ||  : |: |:  |::     ||  |||| |    ||||| |:| : |
Db          1 QDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56

Qy         60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104


RESULT 8
US-09-394-268-2
; Sequence 2, Application US/09394268
; Patent No. 6175003
; GENERAL INFORMATION:
;  APPLICANT: Saxena, Shailendra K
;  TITLE OF INVENTION: NUCLEIC ACIDS ENCODING RIBONUCLEASES AND METHODS OF
;  TITLE OF INVENTION: MAKING THEM
;  FILE REFERENCE: 5013
;  CURRENT APPLICATION NUMBER: US/09/394,268
;  CURRENT FILING DATE: 1999-09-10
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 104
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: SEQ ID NO:1 with Leu at position 23 and Cys at
;   OTHER INFORMATION: position 72
US-09-394-268-2

  Query Match             45.2%;  Score 273.5;  DB 3;  Length 104;
  Best Local Similarity   49.5%;  Pred. No. 2.8e-24;
  Matches   55;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          2 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 59
              |:| |||:||| ||  : |: ||  |::     ||  |||| |    ||||| |:| : |
Db          1 QDWLTFQKKHITNTRDVDCDNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56

Qy         60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
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Db         57 VLTTSEFYLSDC---NVTCRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104


RESULT 9
US-09-687-748-1
; Sequence 1, Application US/09687748
; Patent No. 6423515
; GENERAL INFORMATION:
;  APPLICANT:  Saxena, Shailendra K
;  TITLE OF INVENTION:  METHODS OF MAKING NUCLEIC ACIDS ENCODING RIBONUCLEASES
;  FILE REFERENCE:  5013 US 01
;  CURRENT APPLICATION NUMBER: US/09/687,748
;  CURRENT FILING DATE:  2000-10-14
;  PRIOR APPLICATION NUMBER:  09/394,268
;  PRIOR FILING DATE:  1999-09-10
;  NUMBER OF SEQ ID NOS:  8
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 104
;   TYPE: PRT
;   ORGANISM: Rana pipiens
US-09-687-748-1

  Query Match             45.2%;  Score 273.5;  DB 4;  Length 104;
  Best Local Similarity   48.6%;  Pred. No. 2.8e-24;
  Matches   54;  Conservative   16;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          2 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 59
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;      DEVELOPMENTAL STAGE:  Oocyte
US-08-467-955-2

  Query Match             46.4%;  Score 280.5;  DB 1;  Length 104;
  Best Local Similarity   48.6%;  Pred. No. 4.4e-25;
  Matches   54;  Conservative   17;  Mismatches   31;  Indels    9;  Gaps    4;

Qy          2 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 59
              ::| |||:||: ||  : || |:  |::     ||  |||| |    ||||| |:| : |
Db          1 EDWLTFQKKHVTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56

Qy         60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:|||
Db         57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGRC 104


RESULT 4
US-08-875-811-39
; Sequence 39, Application US/08875811
; Patent No. 6045793
;  GENERAL INFORMATION:
;    APPLICANT:  Rybak, Susanna M.
;    APPLICANT:  Newton, Dianne L.
;    APPLICANT:  Boque, Lluis
;    APPLICANT:  Wlodawer, Alexander
;    TITLE OF INVENTION:  Recombinant Ribonuclease Proteins
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/875,811
;      FILING DATE:  19-FEB-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/02588
;      FILING DATE:  19-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/011,800
;      FILING DATE:  21-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Faris, Susan K.
;      REGISTRATION NUMBER:  41,739
;      REFERENCE/DOCKET NUMBER:  015280-244100US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  39:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  105 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-875-811-39

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  Best Local Similarity   48.2%;  Pred. No. 1.7e-24;
  Matches   54;  Conservative   17;  Mismatches   32;  Indels    9;  Gaps    4;

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              |::| |||:||| ||  : |: |:  |::     ||  |||| |    ||||| |:| :
Db          1 MEDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASK 56

Qy         59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
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Db         57 NVLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 105


RESULT 5
US-08-875-811-41
; Sequence 41, Application US/08875811
; Patent No. 6045793
;  GENERAL INFORMATION:
;    APPLICANT:  Rybak, Susanna M.
;    APPLICANT:  Newton, Dianne L.
;    APPLICANT:  Boque, Lluis
;    APPLICANT:  Wlodawer, Alexander
;    TITLE OF INVENTION:  Recombinant Ribonuclease Proteins
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/875,811
;      FILING DATE:  19-FEB-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/02588
;      FILING DATE:  19-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/011,800
;      FILING DATE:  21-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Faris, Susan K.
;      REGISTRATION NUMBER:  41,739
;      REFERENCE/DOCKET NUMBER:  015280-244100US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  41:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  355 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-875-811-41

  Query Match             45.5%;  Score 275.5;  DB 3;  Length 355;
  Best Local Similarity   48.2%;  Pred. No. 7.4e-24;
  Matches   54;  Conservative   17;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          1 MQNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NL 58
              |::| |||:||| ||  : |: |:  |::     ||  |||| |    ||||| |:| :
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Qy         59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
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Db        307 NVLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 355


RESULT 6
US-08-875-811-51
; Sequence 51, Application US/08875811
; Patent No. 6045793
;  GENERAL INFORMATION:
;    APPLICANT:  Rybak, Susanna M.
;    APPLICANT:  Newton, Dianne L.
;    APPLICANT:  Boque, Lluis
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;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  Protein
;      LOCATION:  1..111
;      OTHER INFORMATION:  /note= "Frog Lectin from Rana
;      OTHER INFORMATION:  catesbeiana"
US-08-891-848-12

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  Best Local Similarity   96.4%;  Pred. No. 5.9e-60;
  Matches  107;  Conservative    3;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          2 QNWATFQQKHIINTPII-CNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 60
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Qy         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
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Db         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111


RESULT 2
US-08-875-811-8
; Sequence 8, Application US/08875811
; Patent No. 6045793
;  GENERAL INFORMATION:
;    APPLICANT:  Rybak, Susanna M.
;    APPLICANT:  Newton, Dianne L.
;    APPLICANT:  Boque, Lluis
;    APPLICANT:  Wlodawer, Alexander
;    TITLE OF INVENTION:  Recombinant Ribonuclease Proteins
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/875,811
;      FILING DATE:  19-FEB-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/02588
;      FILING DATE:  19-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/011,800
;      FILING DATE:  21-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Faris, Susan K.
;      REGISTRATION NUMBER:  41,739
;      REFERENCE/DOCKET NUMBER:  015280-244100US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  111 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  Protein
;      LOCATION:  1..111
;      OTHER INFORMATION:  /note= "Frog Lectin from Rana
;      OTHER INFORMATION:  catesbeiana"
US-08-875-811-8

  Query Match             96.3%;  Score 582.5;  DB 3;  Length 111;
  Best Local Similarity   96.4%;  Pred. No. 5.9e-60;
  Matches  107;  Conservative    3;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          2 QNWATFQQKHIINTPII-CNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 60
              :|||||||||||||||| |||:|||||||||||||||||||||||||||||||||:||
Db          1 ENWATFQQKHIINTPIINCNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60

Qy         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111


RESULT 3
US-08-467-955-2
; Sequence 2, Application US/08467955
; Patent No. 5728805
;  GENERAL INFORMATION:
;    APPLICANT:  Ardelt Ph.D, Wojciech J.
;    TITLE OF INVENTION:  PHARMACEUTICALS AND METHOD FOR MAKING THEM
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mark H. Jay, P.A.
;      STREET:  P.O. Box E
;      CITY:  Short Hills
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07078-0383
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/467,955
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/178,118
;      FILING DATE:  06-APR-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/436,141
;      FILING DATE:  13-NOV-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/814,332
;      FILING DATE:  03-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/283,970
;      FILING DATE:  01-AUG-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jay, Mark H.
;      REGISTRATION NUMBER:  27507
;      REFERENCE/DOCKET NUMBER:  5007 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-912-9066
;      TELEFAX:  201-912-0442
;      TELEX:  No. 5728805 Applicable
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  104 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  N
;    ANTI-SENSE:  N
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  Rana pipiens
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 7, 2004, 21:28:45 ; Search time 12.8756 Seconds
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Title: US-09-961-400-21
Perfect score: 605
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	582.5	96.3	111	2	US-08-891-848-12	Sequence 12, Appl
2	582.5	96.3	111	3	US-08-875-811-8	Sequence 8, Appli
3	280.5	46.4	104	1	US-08-467-955-2	Sequence 2, Appli
4	275.5	45.5	105	3	US-08-875-811-39	Sequence 39, Appl
5	275.5	45.5	355	3	US-08-875-811-41	Sequence 41, Appl
6	275.5	45.5	358	3	US-08-875-811-51	Sequence 51, Appl
7	273.5	45.2	104	3	US-09-394-268-1	Sequence 1, Appli
8	273.5	45.2	104	3	US-09-394-268-2	Sequence 2, Appli
9	273.5	45.2	104	4	US-09-687-748-1	Sequence 1, Appli
10	273.5	45.2	104	4	US-09-687-748-2	Sequence 2, Appli
11	273.5	45.2	104	4	US-08-626-288-1	Sequence 1, Appli
12	273.5	45.2	104	4	US-09-095-429-1	Sequence 1, Appli
13	273.5	45.2	112	3	US-08-875-811-32	Sequence 32, Appl
14	273.5	45.2	129	3	US-08-875-811-63	Sequence 63, Appl
15	273.5	45.2	251	3	US-08-875-811-59	Sequence 59, Appl
16	273.5	45.2	254	3	US-08-875-811-61	Sequence 61, Appl
17	273.5	45.2	355	3	US-08-875-811-49	Sequence 49, Appl
18	273.5	45.2	355	3	US-08-875-811-57	Sequence 57, Appl
19	273.5	45.2	355	3	US-08-875-811-64	Sequence 64, Appl
20	273.5	45.2	366	3	US-08-875-811-55	Sequence 55, Appl
21	273.5	45.2	379	3	US-08-875-811-43	Sequence 43, Appl
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28	268.5	44.4	104	3	US-08-875-811-1	Sequence 1, Appli
29	268.5	44.4	104	4	US-09-071-672-1	Sequence 1, Appli
30	268.5	44.4	104	4	US-09-986-119-1	Sequence 1, Appli
31	268.5	44.4	105	3	US-08-875-811-26	Sequence 26, Appl
32	268.5	44.4	106	3	US-08-875-811-28	Sequence 28, Appl
33	268.5	44.4	107	3	US-08-875-811-30	Sequence 30, Appl
34	267.5	44.2	105	3	US-08-875-811-24	Sequence 24, Appl
35	264.5	43.7	358	3	US-08-875-811-45	Sequence 45, Appl
36	264.5	43.7	365	3	US-08-875-811-53	Sequence 53, Appl
37	246.5	40.7	107	3	US-08-875-811-20	Sequence 20, Appl
38	235.5	38.9	111	3	US-08-875-811-22	Sequence 22, Appl
39	232	38.3	114	3	US-09-223-118-3	Sequence 3, Appli
40	228.5	37.8	360	3	US-08-875-811-47	Sequence 47, Appl
41	223	36.9	114	3	US-09-223-118-2	Sequence 2, Appli
42	222	36.7	114	3	US-09-223-118-1	Sequence 1, Appli
43	221	36.5	114	3	US-09-223-118-4	Sequence 4, Appli
44	202	33.4	83	3	US-08-875-811-2	Sequence 2, Appli
45	202	33.4	83	4	US-09-071-672-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-891-848-12
; Sequence 12, Application US/08891848
; Patent No. 5955073
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Youle, Richard J.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Nicholls, Peter J.
; TITLE OF INVENTION: Selective RNase Cytotoxic Reagents
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,848
; FILING DATE: No. 5955073 yet assigned
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/125,462
; FILING DATE: 22-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/014,082
; FILING DATE: 04-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/779,195
; FILING DATE: 22-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/510,696
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-110310US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid

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OS   Rana pipiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
FT                   /note= "Met not found in wild type RaPLR1"
FT   Misc-difference 2
FT                   /note= "Wild type Gln replaced with Ser"
XX
PN   WO9950398-A2.
XX
PD   07-OCT-1999.
XX
PF   26-MAR-1999;   99WO-US006641.
XX
PR   27-MAR-1998;   98US-0079751P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL;
XX
DR   WPI; 1999-610847/52.
DR   N-PSDB; AAZ08129.
XX
PT   New recombinant ribonucleases, used for killing target cells, e.g. for
PT   treating cancers, viral infections or autoimmune diseases.
XX
PS   Claim 34; Page 61; 71pp; English.
XX
CC   The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1)
CC   protein with Met at position 1 and Gln2Ser. Carboxy terminal end of
CC   recombinant RaPLR1 has a covalently bound ligand binding moiety, which
CC   can be a LL2 antibody directed against CD22 on cancerous B cells or human
CC   chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells.
CC   Recombinant ribonucleases can be expressed in bacteria without an N-
CC   terminal methionine due to the presence of a signal peptide that is
CC   cleaved by bacteria. The soluble expression of ribonuclease allows the
CC   proteins to be fused in-frame with ligand binding moieties to form
CC   cytotoxic fusion proteins. They can be used for treatment of cancer and
CC   autoimmune diseases
XX
SQ   Sequence 105 AA;

  Query Match             45.9%;  Score 277.5;  DB 2;  Length 105;
  Best Local Similarity   48.2%;  Pred. No. 1.9e-23;
  Matches   54;  Conservative   16;  Mismatches   33;  Indels    9;  Gaps    4;

Qy          1 MQNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NL 58
              | :| |||:||: ||  : || |:  |::     ||  |||| |    |||| |:| :
Db          1 MSDWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASK 56

Qy         59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              |||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         57 NVLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105


RESULT 15
AAY28879
ID   AAY28879 standard; protein; 127 AA.
XX
AC   AAY28879;
XX
DT   25-JAN-2000  (first entry)
XX
DE   Rana pipiens Clone 5a1b ribonuclease.
XX
KW   Rana pipiens ribonuclease Clone 5a1b; RaPLR1; covalently bound; RNase;
KW   LL2 antibody; ligand binding moiety; CD22; cancerous B cell; onconase;
KW   Kaposi's Sarcoma; human chorionic gonadotrophin; hCG; cancer;
KW   recombinant ribonuclease; frog; signal peptide; cytotoxic fusion protein;
KW   autoimmune disease.
XX
OS   Rana pipiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /label= Signal_peptide
FT                   /note= "Putative"
FT   Protein         24. .127
FT                   /label= Rana_pipiens_Clone_5a1b_ribonuclease
XX
PN   WO9950398-A2.
XX
PD   07-OCT-1999.
XX
PF   26-MAR-1999;   99WO-US006641.
XX
PR   27-MAR-1998;   98US-0079751P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL;
XX
DR   WPI; 1999-610847/52.
DR   N-PSDB; AAZ08136.
XX
PT   New recombinant ribonucleases, used for killing target cells, e.g. for
PT   treating cancers, viral infections or autoimmune diseases.
XX
PS   Disclosure; Page 69; 71pp; English.
XX
CC   The present sequence is a Rana pipiens Clone 5a1b ribonuclease (RaPLR1).
CC   It is encoded by Clone 5a1b cDNA obtained from Rana pipiens liver mRNA
CC   library. It exhibits differences with Onconase (RTM) at amino acid
CC   residues 11, 20, 85 and 103. Carboxy terminal end of RaPLR1 has a
CC   covalently bound ligand binding moiety, which can be a LL2 antibody
CC   directed against CD22 on cancerous B cells or human chorionic
CC   gonadotrophin (hCG) effective against Kaposi's Sarcoma cells. Recombinant
CC   ribonucleases can be expressed in bacteria without an N-terminal
CC   methionine due to the presence of a signal peptide that is cleaved by
CC   bacteria. The soluble expression of ribonuclease allows the proteins to
CC   be fused in-frame with ligand binding moieties to form cytotoxic fusion
CC   proteins. They can be used for treatment of cancer and autoimmune
CC   diseases
XX
SQ   Sequence 127 AA;

  Query Match             45.9%;  Score 277.5;  DB 2;  Length 127;
  Best Local Similarity   48.6%;  Pred. No. 2.4e-23;
  Matches   54;  Conservative   16;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          2 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 59
              |:| |||:||: ||  : || |:  |::     ||  |||| |    |||| |:| : |
Db         24 QDWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 79

Qy         60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         80 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 127


Search completed: May  7, 2004, 21:38:29
Job time : 47.3489 secs
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AC   AAY39400;
XX
DT   01-DEC-1999  (first entry)
XX
DE   Recombinant frog Onconase.
XX
KW   Ribonuclease; protein synthesis; inhibition; cancer; cytotoxic.
XX
OS   Rana pipiens.
XX
PN   WO9946389-A1.
XX
PD   16-SEP-1999.
XX
PF   11-MAR-1999;   99WO-US004252.
XX
PR   11-MAR-1998;   98US-0077557P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Goldenberg DM,  Hansen H,  Leung S;
XX
DR   WPI; 1999-551416/46.
DR   N-PSDB; AAZ19767.
XX
PT   A new recombinant Onconase used to treat, e.g. colon cancer.
XX
PS   Example 1; Fig 1; 42pp; English.
XX
CC   This sequence represents recombinant frog Onconase. Onconase has
CC   ribonuclease and anti-tumour activity. The cDNA was produced via PCR
CC   (using primers AAZ19768-Z19769) of two synthetic DNAs whose sequences
CC   encoded most of the N-terminal or the C-terminal amino acids of mature
CC   Onconase. The two PCR products generated encoded either the N-terminal 54
CC   amino acids (minus the initial methionine) or the C-terminal 51 amino
CC   acids, and were ligated in frame at an NruI site. The cDNA was then
CC   subcloned into a vector e.g., pBluescript, where the ATG initiation codon
CC   was ligated to the cDNA. After expression in E. coli, the recombinant
CC   protein was purified. The initial N-formyl methionine was cleaved off and
CC   the now N-terminal glutamate residue cyclised to form an N-terminal
CC   pyroglutamate. The pyroglutamate residue forms part of the phosphate
CC   binding pocket of Onconaseand is essential for both ribonuclease and anti
CC   -tumour activity. Onconase is a 12 kD ribonuclease which causes cell
CC   death as a result of potent inhibition of protein synthesis by a
CC   mechanism involving inactivation of cellular RNA. It is not inhibited by
CC   mammalian placental ribonuclease inhibitor, which may explain its
CC   enhanced cytotoxicity relative to mammalian enzymes. It has anti-tumour
CC   activity against a variety of solid tumours e.g, colon or pancreatic
CC   cancers, and can be used alone or in combination with other anti-cancer
CC   agents such as tamoxifen. When used as an anti-tumour agent, Onconase can
CC   be conjugated to a marker which targets it to a specific cell type
XX
SQ   Sequence 105 AA;

  Query Match             46.0%;  Score 278.5;  DB 2;  Length 105;
  Best Local Similarity   49.1%;  Pred. No. 1.5e-23;
  Matches   55;  Conservative   16;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          1 MQNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NL 58
              ||:| |||:||| ||  : |: |:  |::     ||  |||| |    ||||| |:| :
Db          1 MQDWLTFQKKHITNTKDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASK 56

Qy         59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              |||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         57 NVLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 105


RESULT 13
AAY28865
ID   AAY28865 standard; protein; 104 AA.
XX
AC   AAY28865;
XX
DT   25-JAN-2000  (first entry)
XX
DE   Rana pipiens liver ribonuclease (RaPLR1).
XX
KW   Rana pipiens liver ribonuclease; RaPLR1; covalently bound; LL2 antibody;
KW   ligand binding moiety; CD22; cancerous B cell; Kaposi's Sarcoma; frog;
KW   human chorionic gonadotrophin; hCG; recombinant ribonuclease; RNase;
KW   signal peptide; cytotoxic fusion protein; cancer; autoimmune disease.
XX
OS   Rana pipiens.
XX
PN   WO9950398-A2.
XX
PD   07-OCT-1999.
XX
PF   26-MAR-1999;   99WO-US006641.
XX
PR   27-MAR-1998;   98US-0079751P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL;
XX
DR   WPI; 1999-610847/52.
DR   N-PSDB; AAZ08124.
XX
PT   New recombinant ribonucleases, used for killing target cells, e.g. for
PT   treating cancers, viral infections or autoimmune diseases.
XX
PS   Claim 1; Page 55; 71pp; English.
XX
CC   The present sequence is Rana pipiens liver ribonuclease (RaPLR1) protein.
CC   Carboxy terminal end of RaPLR1 has a covalently bound ligand binding
CC   moiety, which can be a LL2 antibody directed against CD22 on cancerous B
CC   cells or human chorionic gonadotrophin (hCG) effective against Kaposi's
CC   Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria
CC   without an N-terminal methionine due to the presence of a signal peptide
CC   that is cleaved by bacteria. The soluble expression of ribonuclease
CC   allows the proteins to be fused in-frame with ligand binding moieties to
CC   form cytotoxic fusion proteins. They can be used for treatment of cancer
CC   and autoimmune diseases
XX
SQ   Sequence 104 AA;

  Query Match             45.9%;  Score 277.5;  DB 2;  Length 104;
  Best Local Similarity   48.6%;  Pred. No. 1.9e-23;
  Matches   54;  Conservative   16;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          2 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 59
              |:| |||:||: ||  : || |:  |::     ||  |||| |    ||||| |:| : |
Db          1 QDWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56

Qy         60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104


RESULT 14
AAY28871
ID   AAY28871 standard; protein; 105 AA.
XX
AC   AAY28871;
XX
DT   25-JAN-2000  (first entry)
XX
DE   Recombinant Met(-1) RaPLR1 Gln1Ser amino acid sequence.
XX
KW   Recombinant Met(-1) Rana pipiens ribonuclease Gln1Ser; RaPLR1; CD22;
KW   covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
KW   Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
KW   recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
KW   autoimmune disease; RNase.
XX
```

```
SQ   Sequence 105 AA;

  Query Match             46.7%;  Score 282.5;  DB 2;  Length 105;
  Best Local Similarity   49.1%;  Pred. No. 5.2e-24;
  Matches   55;  Conservative   16;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          1 MQNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NL 58
              ||:| |||:||: ||  : || |:  |::     ||  |||| |    |||||:|| :
Db          1 MQDWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASK 56

Qy         59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              |||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         57 NVLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105


RESULT 10
AAW06544
ID   AAW06544 standard; protein; 104 AA.
XX
AC   AAW06544;
XX
DT   22-AUG-1997  (first entry)
XX
DE   Antitumour protein from Rana pipiens oocytes.
XX
KW   Tumour; chemotherapy; radiotherapy; frog.
XX
OS   Rana pipiens.
XX
PN   WO9639428-A1.
XX
PD   12-DEC-1996.
XX
PF   03-JUN-1996;   96WO-US008304.
XX
PR   06-JUN-1995;   95US-00467955.
XX
PA   (ALFA-) ALFACELL CORP.
XX
PI   Ardelt WJ;
XX
DR   WPI; 1997-043063/04.
XX
PT   Antitumour proteins from Rana pipiens oocyte(s) - have fewer
PT   disadvantages than chemotherapy, surgery and radiotherapy.
XX
PS   Claim 8; Page 28; 45pp; English.
XX
CC   The present sequence is a specifically claimed example of an antitumour
CC   protein from the generic protein in AAW18224, with the molecular weight
CC   12000. This is one of two preferred proteins (the other in AAW06543) that
CC   have been isolated from Rana pipiens oocytes. Both proteins have a
CC   blocked amino terminal group and are essentially free of carbohydrates.
CC   The proteins are used to treat tumours. Use of the peptides has fewer
CC   disadvantages than chemotherapy, radiotherapy and surgery in the
CC   treatment of tumours
XX
SQ   Sequence 104 AA;

  Query Match             46.4%;  Score 280.5;  DB 2;  Length 104;
  Best Local Similarity   48.6%;  Pred. No. 8.7e-24;
  Matches   54;  Conservative   17;  Mismatches   31;  Indels    9;  Gaps    4;

Qy          2 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 59
              ::| |||:||: ||  : || |:  |::     ||  |||| |    |||||:|| : |
Db          1 EDWLTFQKKHVTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56

Qy         60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:|||
Db         57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGRC 104


RESULT 11
AAY28866
ID   AAY28866 standard; protein; 104 AA.
XX
AC   AAY28866;
XX
DT   25-JAN-2000  (first entry)
XX
DE   Recombinant RaPLR1 Met23Leu amino acid sequence.
XX
KW   Recombinant Rana pipiens ribonuclease; RaPLR1 Met23Leu; covalently bound;
KW   LL2 antibody; ligand binding moiety; CD22; cancerous B cell; RNase;
KW   Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
KW   recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
KW   autoimmune disease.
XX
OS   Rana pipiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 23
FT                   /note= "Wild type Met replaced with Leu"
XX
PN   WO9950398-A2.
XX
PD   07-OCT-1999.
XX
PF   26-MAR-1999;   99WO-US006641.
XX
PR   27-MAR-1998;   98US-0079751P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL;
XX
DR   WPI; 1999-610847/52.
DR   N-PSDB; AAZ08125.
XX
PT   New recombinant ribonucleases, used for killing target cells, e.g. for
PT   treating cancers, viral infections or autoimmune diseases.
XX
PS   Claim 34; Page 56; 71pp; English.
XX
CC   The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1)
CC   protein with Met23Leu. Carboxy terminal end of recombinant RaPLR1 has a
CC   covalently bound ligand binding moiety, which can be a LL2 antibody
CC   directed against CD22 on cancerous B cells or human chorionic
CC   gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant
CC   ribonucleases can be expressed in bacteria without an N-terminal
CC   methionine due to the presence of a signal peptide that is cleaved by
CC   bacteria. The soluble expression of ribonuclease allows the proteins to
CC   be fused in-frame with ligand binding moieties to form cytotoxic fusion
CC   proteins. They can be used for treatment of cancer and autoimmune
CC   diseases
XX
SQ   Sequence 104 AA;

  Query Match             46.2%;  Score 279.5;  DB 2;  Length 104;
  Best Local Similarity   49.5%;  Pred. No. 1.1e-23;
  Matches   55;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          2 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 59
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Db          1 QDWLTFQKKHLTNTRDVDCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56

Qy         60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104


RESULT 12
AAY39400
ID   AAY39400 standard; protein; 105 AA.
XX
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CC   (Rana catesbeiana) lectin used to describe the method of the invention
XX
SQ   Sequence 111 AA;

  Query Match             96.3%;  Score 582.5;  DB 2;  Length 111;
  Best Local Similarity   96.4%;  Pred. No. 6.3e-58;
  Matches  107;  Conservative    3;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          2 QNWATFQQKHIINTPII-CNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 60
              :|||||||||||||||| ||||:|||||||||||||||||||||||||||||:||
Db          1 ENWATFQQKHIINTPIINCNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60

Qy         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111


RESULT 8
AAY28869
ID   AAY28869 standard; protein; 105 AA.
XX
AC   AAY28869;
XX
DT   25-JAN-2000  (first entry)
XX
DE   Recombinant Met(-1) RaPLR1 Met23Leu-(His)6 protein.
XX
KW   Recombinant Met(-1) Rana pipiens ribonuclease Met23Leu-(His)6; RaPLR1;
KW   CD22; covalently bound; LL2 antibody; ligand binding moiety; RNase;
KW   cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG;
KW   signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
KW   cancer; frog; autoimmune disease.
XX
OS   Rana pipiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
FT                   /note= "Met not found in wild type RaPLR1"
FT   Misc-difference 1
FT                   /note= "(His)6 histidine tag attached to N-terminal Met"
FT   Misc-difference 24
FT                   /note= "Wild type Met replaced with Leu"
XX
PN   WO9950398-A2.
XX
PD   07-OCT-1999.
XX
PF   26-MAR-1999;   99WO-US006641.
XX
PR   27-MAR-1998;   98US-0079751P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL;
XX
DR   WPI; 1999-610847/52.
DR   N-PSDB; AAZ08127.
XX
PT   New recombinant ribonucleases, used for killing target cells, e.g. for
PT   treating cancers, viral infections or autoimmune diseases.
XX
PS   Claim 4; Page 59; 71pp; English.
XX
CC   The present sequence is a recombinant Rana pipiens ribonuclease protein
CC   (RaPLR1) with Met at position 1 attached to (His)6 tag and Met24Leu.
CC   Carboxy terminal end of recombinant RaPLR1 has a covalently bound ligand
CC   binding moiety, which can be a LL2 antibody directed against CD22 on
CC   cancerous B cells or human chorionic gonadotrophin (hCG) effective
CC   against Kaposi's sarcoma cells. Recombinant ribonucleases can be
CC   expressed in bacteria without an N-terminal methionine due to the
CC   presence of a signal peptide that is cleaved by bacteria. The soluble
CC   expression of ribonuclease allows the proteins to be fused in-frame with
CC   ligand binding moieties to form cytotoxic fusion proteins. They can be
CC   used for treatment of cancer and autoimmune diseases
XX
SQ   Sequence 105 AA;

  Query Match             47.0%;  Score 284.5;  DB 2;  Length 105;
  Best Local Similarity   50.0%;  Pred. No. 3.1e-24;
  Matches   56;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          1 MQNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NL 58
              ||:| |||:||: ||  : || ||  |::     ||  |||| |    ||||| |:| :
Db          1 MQDWLTFQKKHLTNTRDVDCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASK 56

Qy         59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              |||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         57 NVLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105


RESULT 9
AAY28867
ID   AAY28867 standard; protein; 105 AA.
XX
AC   AAY28867;
XX
DT   25-JAN-2000  (first entry)
XX
DE   Recombinant Met(-1) RaPLR1.
XX
KW   Recombinant Met(-1) Rana pipiens ribonuclease; RaPLR1; CD22; RNase;
KW   covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
KW   Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
KW   recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
KW   autoimmune disease.
XX
OS   Rana pipiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
FT                   /note= "Met not found in wild type RaPLR1"
XX
PN   WO9950398-A2.
XX
PD   07-OCT-1999.
XX
PF   26-MAR-1999;   99WO-US006641.
XX
PR   27-MAR-1998;   98US-0079751P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL;
XX
DR   WPI; 1999-610847/52.
DR   N-PSDB; AAZ08126.
XX
PT   New recombinant ribonucleases, used for killing target cells, e.g. for
PT   treating cancers, viral infections or autoimmune diseases.
XX
PS   Claim 34; Page 57; 71pp; English.
XX
CC   The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1)
CC   protein with Met at position 1. Carboxy terminal end of recombinant
CC   RaPLR1 has a covalently bound ligand binding moiety, which can be a LL2
CC   antibody directed against CD22 on cancerous B cells or human chorionic
CC   gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant
CC   ribonucleases can be expressed in bacteria without an N-terminal
CC   methionine due to the presence of a signal peptide that is cleaved by
CC   bacteria. The soluble expression of ribonuclease allows the proteins to
CC   be fused in-frame with ligand binding moieties to form cytotoxic fusion
CC   proteins. They can be used for treatment of cancer and autoimmune
CC   diseases
XX
```

```
CC   autoimmune diseases
XX
SQ   Sequence 111 AA;

  Query Match             98.5%;  Score 596;  DB 2;  Length 111;
  Best Local Similarity   97.3%;  Pred. No. 1.9e-59;
  Matches  108;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MQNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 60
              |:|||||||||||||||||:|||||||||||||||||||||||||||||||||||:||
Db          1 MSNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60

Qy         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111


RESULT 6
AAY28877
ID   AAY28877 standard; protein; 110 AA.
XX
AC   AAY28877;
XX
DT   25-JAN-2000  (first entry)
XX
DE   Recombinant RaCOR1 Gln1Ser amino acid sequence.
XX
KW   Recombinant Rana catesbeiana oocyte ribonuclease; RaCOR1 Gln1Ser; CD22;
KW   covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
KW   bullfrog; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; RNase;
KW   signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
KW   cancer; autoimmune disease.
XX
OS   Rana catesbeiana.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
FT                   /note= "Wild type Gln replaced with Ser"
XX
PN   WO9950398-A2.
XX
PD   07-OCT-1999.
XX
PF   26-MAR-1999;   99WO-US006641.
XX
PR   27-MAR-1998;   98US-0079751P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL;
XX
DR   WPI; 1999-610847/52.
DR   N-PSDB; AAZ08134.
XX
PT   New recombinant ribonucleases, used for killing target cells, e.g. for
PT   treating cancers, viral infections or autoimmune diseases.
XX
PS   Claim 22; Page 67; 71pp; English.
XX
CC   The present sequence is a recombinant Rana catesbeiana oocyte
CC   ribonuclease (RaCOR1) protein with Gln1Ser. Carboxy terminal end of
CC   recombinant RaCOR1 has a covalently bound ligand binding moiety, which
CC   can be a LL2 antibody directed against CD22 on cancerous B cells or human
CC   chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells.
CC   Recombinant ribonucleases can be expressed in bacteria without an N-
CC   terminal methionine due to the presence of a signal peptide that is
CC   cleaved by bacteria. The soluble expression of ribonuclease allows the
CC   proteins to be fused in-frame with ligand binding moieties to form
CC   cytotoxic fusion proteins. They can be used for treatment of cancer and
CC   autoimmune diseases
XX
SQ   Sequence 110 AA;

  Query Match             97.7%;  Score 591;  DB 2;  Length 110;
  Best Local Similarity   98.2%;  Pred. No. 6.8e-59;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 NWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVLS 62
              |||||||||||||||||||:|||||||||||||||||||||||||||||||:||||
Db          2 NWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS 61

Qy         63 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110


RESULT 7
AAY33321
ID   AAY33321 standard; protein; 111 AA.
XX
AC   AAY33321;
XX
DT   29-NOV-1999  (first entry)
XX
DE   Frog lectin protein fragment.
XX
KW   Cytotoxic; RNase; ribonuclease; pancreatic; antibody; light chain;
KW   heavy chain; cell surface marker; treatment; tumor; viral infection;
KW   parasite infection; immune dysfunctional cell; autoimmune disease;
KW   contraceptive; cell separation; transplantation; bone marrow ablation;
KW   leukemia cell; T-cell; graft-versus-host disease; bullfrog; lectin.
XX
OS   Rana catesbeiana.
XX
PN   US5955073-A.
XX
PD   21-SEP-1999.
XX
PF   09-JUL-1997;   97US-00891848.
XX
PR   20-APR-1990;   90US-00510696.
PR   22-OCT-1991;   91US-00779195.
PR   04-FEB-1993;   93US-00014082.
PR   22-SEP-1993;   93US-00125462.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL,  Nicholls PJ,  Youle RJ;
XX
DR   WPI; 1999-560488/47.
XX
PT   Recombinantly fused pancreatic RNase-targeting proteins useful for
PT   treating tumors, infections, immune or autoimmune disorders and as a
PT   contraceptive.
XX
PS   Example 3; Fig 19; 47pp; English.
XX
CC   This invention describes a novel nucleic acid construct comprising
CC   sequences encoding functional pancreatic RNase and a second protein
CC   (preferably the light and heavy chains of an antibody) which binds a
CC   specific cell surface marker on a target cell and functions as a
CC   cytotoxic agent. The products can be used for selectively killing cells
CC   expressing a specific surface marker. They can be used for treating
CC   tumors or infected cells (e.g. cells infected by viruses (especially
CC   latent or chronic virus infections, such as human immunodeficiency virus
CC   (HIV)-1, Epstein-Barr virus, herpes viruses (herpes simplex types I and
CC   II), hepatitis viruses (B, non-A-non-B, and delta), herpes zoster,
CC   cytomegalovirus)) and cells infected with parasites (such as the malaria
CC   parasite)). They can also be used for treating immune dysfunctional cells
CC   in immune and autoimmune diseases. Additionally, they may be used as
CC   contraceptives. Finally they can also be used for cell separation in
CC   vitro by selectively killing unwanted types of cells (e.g. in bone
CC   marrow) prior to transplantation into a patient undergoing marrow
CC   ablation by radiation or for killing leukemia cells or T-cells that would
CC   cause graft-versus-host disease. This sequence represents a bullfrog
```

CC end of recombinant RaCOR1 has a covalently bound ligand binding moiety,
CC which can be a LL2 antibody directed against CD22 on cancerous B cells or
CC human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma
CC cells. Recombinant ribonucleases can be expressed in bacteria without an
CC N-terminal methionine due to the presence of a signal peptide that is
CC cleaved by bacteria. The soluble expression of ribonuclease allows the
CC proteins to be fused in-frame with ligand binding moieties to form
CC cytotoxic fusion proteins. They can be used for treatment of cancer and
CC autoimmune diseases
XX
SQ Sequence 110 AA;

Query Match 99.2%; Score 600; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 6.5e-60;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 61
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 QNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 60

Qy 62 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 4
AAY28872
ID AAY28872 standard; protein; 110 AA.
XX
AC AAY28872;
XX
DT 25-JAN-2000 (first entry)
XX
DE Rana catesbeiana oocyte ribonuclease (RaCOR1) amino acid sequence.
XX
KW Rana catesbeiana oocyte ribonuclease; RaCOR1; covalently bound; CD22;
KW LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's Sarcoma;
KW human chorionic gonadotrophin; hCG; recombinant ribonuclease; bullfrog;
KW signal peptide; cytotoxic fusion protein; cancer; autoimmune disease;
KW RNase.
XX
OS Rana catesbeiana.
OS Synthetic.
XX
PN WO9950398-A2.
XX
PD 07-OCT-1999.
XX
PF 26-MAR-1999; 99WO-US006641.
XX
PR 27-MAR-1998; 98US-0079751P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rybak SM, Newton DL;
XX
DR WPI; 1999-610847/52.
DR N-PSDB; AAZ08130.
XX
PT New recombinant ribonucleases, used for killing target cells, e.g. for
PT treating cancers, viral infections or autoimmune diseases.
XX
PS Claim 22; Page 62; 71pp; English.
XX
CC The present sequence is a Rana catesbeiana oocyte ribonuclease (RaCOR1)
CC protein encoded by a cDNA modified for expression in E. coli. Carboxy
CC terminal end of RaCOR1 has a covalently bound ligand binding moiety,
CC which can be a LL2 antibody directed against CD22 on cancerous B cells or
CC human chorionic gonadotrophin (hCG) effective against Kaposi's Sarcoma
CC cells. Recombinant ribonucleases can be expressed in bacteria without an
CC N-terminal methionine due to the presence of a signal peptide that is
CC cleaved by bacteria. The soluble expression of ribonuclease allows the
CC proteins to be fused in-frame with ligand binding moieties to form
CC cytotoxic fusion proteins. They can be used for treatment of cancer and
CC autoimmune diseases
XX
SQ Sequence 110 AA;

Query Match 98.5%; Score 596; DB 2; Length 110;
Best Local Similarity 98.2%; Pred. No. 1.8e-59;
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 61
||||||||||||||||||||:||||||||||||||||||||||||||||:|||
Db 1 QNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 60

Qy 62 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 5
AAY28878
ID AAY28878 standard; protein; 111 AA.
XX
AC AAY28878;
XX
DT 25-JAN-2000 (first entry)
XX
DE Recombinant Met(-1) RaCOR1 Gln1Ser amino acid sequence.
XX
KW Recombinant Met(-1) Rana catesbeiana oocyte ribonuclease Gln1Ser; RaCOR1;
KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
KW Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
KW recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;
KW CD22; RNase; autoimmune disease.
XX
OS Rana catesbeiana.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1
FT /note= "Met not found in wild type RaCOR1"
FT Misc-difference 2
FT /note= "Wild type Gln replaced with Ser"
XX
PN WO9950398-A2.
XX
PD 07-OCT-1999.
XX
PF 26-MAR-1999; 99WO-US006641.
XX
PR 27-MAR-1998; 98US-0079751P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rybak SM, Newton DL;
XX
DR WPI; 1999-610847/52.
DR N-PSDB; AAZ08135.
XX
PT New recombinant ribonucleases, used for killing target cells, e.g. for
PT treating cancers, viral infections or autoimmune diseases.
XX
PS Claim 22; Page 68; 71pp; English.
XX
CC The present sequence is a recombinant Rana catesbeiana ribonuclease
CC (RaCOR1) protein with Met at position 1 and Gln2Ser. Carboxy terminal end
CC of recombinant RaCOR1 has a covalently bound ligand binding moiety, which
CC can be a LL2 antibody directed against CD22 on cancerous B cells or human
CC chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells.
CC Recombinant ribonucleases can be expressed in bacteria without an N-
CC terminal methionine due to the presence of a signal peptide that is
CC cleaved by bacteria. The soluble expression of ribonuclease allows the
CC proteins to be fused in-frame with ligand binding moieties to form
CC cytotoxic fusion proteins. They can be used for treatment of cancer and

```
XX
CC   The present sequence is a recombinant Rana catesbeiana oocyte
CC   ribonuclease (RaCOR1) protein with Met at position 1 attached to a (His)6
CC   tag, Met23Leu and Met58Leu. Carboxy terminal end of recombinant RaCOR1
CC   has a covalently bound ligand binding moiety, which can be a LL2 antibody
CC   directed against CD22 on cancerous B cells or human chorionic
CC   gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant
CC   ribonucleases can be expressed in bacteria without an N-terminal
CC   methionine due to the presence of a signal peptide that is cleaved by
CC   bacteria. The soluble expression of ribonuclease allows the proteins to
CC   be fused in-frame with ligand binding moieties to form cytotoxic fusion
CC   proteins. They can be used for treatment of cancer and autoimmune
CC   diseases
XX
SQ   Sequence 111 AA;

  Query Match             100.0%;  Score 605;  DB 2;  Length 111;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-60;
  Matches  111;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MQNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MQNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 60

Qy         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111


RESULT 2
AAY28873
ID   AAY28873 standard; protein; 111 AA.
XX
AC   AAY28873;
XX
DT   25-JAN-2000  (first entry)
XX
DE   Recombinant Met(-1) RaCOR1.
XX
KW   Recombinant Met(-1) Rana catesbeiana oocyte ribonuclease; RaCOR1; CD22;
KW   covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
KW   Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
KW   recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;
KW   RNase; autoimmune disease.
XX
OS   Rana catesbeiana.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
FT                   /note= "Met not found in wild type RaCOR1"
XX
PN   WO9950398-A2.
XX
PD   07-OCT-1999.
XX
PF   26-MAR-1999;   99WO-US006641.
XX
PR   27-MAR-1998;   98US-0079751P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL;
XX
DR   WPI; 1999-610847/52.
DR   N-PSDB; AAZ08131.
XX
PT   New recombinant ribonucleases, used for killing target cells, e.g. for
PT   treating cancers, viral infections or autoimmune diseases.
XX
PS   Claim 22; Page 63; 71pp; English.
XX
CC   The present sequence is a recombinant Rana catesbeiana oocyte
CC   ribonuclease (RaCOR1) protein with Met at position 1. Carboxy terminal
CC   end of recombinant RaCOR1 has a covalently bound ligand binding moiety,
CC   which can be a LL2 antibody directed against CD22 on cancerous B cells or
CC   human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma
CC   cells. Recombinant ribonucleases can be expressed in bacteria without an
CC   N-terminal methionine due to the presence of a signal peptide that is
CC   cleaved by bacteria. The soluble expression of ribonuclease allows the
CC   proteins to be fused in-frame with ligand binding moieties to form
CC   cytotoxic fusion proteins. They can be used for treatment of cancer and
CC   autoimmune diseases
XX
SQ   Sequence 111 AA;

  Query Match             99.3%;  Score 601;  DB 2;  Length 111;
  Best Local Similarity   98.2%;  Pred. No. 5e-60;
  Matches  109;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MQNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 60
              ||||||||||||||||||||:|||||||||||||||||||||||||||||:||
Db          1 MQNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60

Qy         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111


RESULT 3
AAY28874
ID   AAY28874 standard; protein; 110 AA.
XX
AC   AAY28874;
XX
DT   25-JAN-2000  (first entry)
XX
DE   Recombinant RaCOR1 Met22Leu Met57Leu amino acid sequence.
XX
KW   Recombinant Rana catesbeiana oocyte ribonuclease; covalently bound;
KW   RaCOR1 Met22Leu Met57Leu; LL2 antibody; ligand binding moiety; CD22;
KW   cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG;
KW   signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
KW   cancer; bullfrog; RNase; autoimmune disease.
XX
OS   Rana catesbeiana.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 22
FT                   /note= "Wild type Met replaced with Leu"
FT   Misc-difference 57
FT                   /note= "Wild type Met replaced with Leu"
XX
PN   WO9950398-A2.
XX
PD   07-OCT-1999.
XX
PF   26-MAR-1999;   99WO-US006641.
XX
PR   27-MAR-1998;   98US-0079751P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL;
XX
DR   WPI; 1999-610847/52.
DR   N-PSDB; AAZ08132.
XX
PT   New recombinant ribonucleases, used for killing target cells, e.g. for
PT   treating cancers, viral infections or autoimmune diseases.
XX
PS   Claim 22; Page 64; 71pp; English.
XX
CC   The present sequence is a recombinant Rana catesbeiana oocyte
CC   ribonuclease (RaCOR1) protein with Met22Leu Met57Leu. Carboxy terminal
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 7, 2004, 21:25:55 ; Search time 47.3489 Seconds
(without alignments)
662.376 Million cell updates/sec

Title: US-09-961-400-21
Perfect score: 605
Sequence: 1 MQNWATFQQKHIINTPIICN.....ICVKCENQYPVHFAGIGRCP 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	605	100.0	111	2	AAY28876	Aay28876 Recombina
2	601	99.3	111	2	AAY28873	Aay28873 Recombina
3	600	99.2	110	2	AAY28874	Aay28874 Recombina
4	596	98.5	110	2	AAY28872	Aay28872 Rana cate
5	596	98.5	111	2	AAY28878	Aay28878 Recombina
6	591	97.7	110	2	AAY28877	Aay28877 Recombina
7	582.5	96.3	111	2	AAY33321	Aay33321 Frog lect
8	284.5	47.0	105	2	AAY28869	Aay28869 Recombina
9	282.5	46.7	105	2	AAY28867	Aay28867 Recombina
10	280.5	46.4	104	2	AAW06544	Aaw06544 Antitumou
11	279.5	46.2	104	2	AAY28866	Aay28866 Recombina
12	278.5	46.0	105	2	AAY39400	Aay39400 Recombina
13	277.5	45.9	104	2	AAY28865	Aay28865 Rana pipi
14	277.5	45.9	105	2	AAY28871	Aay28871 Recombina
15	277.5	45.9	127	2	AAY28879	Aay28879 Rana pipi
16	275.5	45.5	105	2	AAW35123	Aaw35123 R. pipien
17	275.5	45.5	355	2	AAW35125	Aaw35125 R. pipien
18	275.5	45.5	358	2	AAW35130	Aaw35130 R. pipien
19	273.5	45.2	104	2	AAW30301	Aaw30301 Recombina
20	273.5	45.2	104	4	AAB31667	Aab31667 Amino aci
21	273.5	45.2	104	4	AAB31666	Aab31666 Amino aci
22	273.5	45.2	104	5	ABG32650	Abg32650 Northern
23	273.5	45.2	104	5	ABG31617	Abg31617 Northern
24	273.5	45.2	112	2	AAW35118	Aaw35118 R. pipien
25	273.5	45.2	251	2	AAW35134	Aaw35134 R. pipien
26	273.5	45.2	254	2	AAW35135	Aaw35135 R. pipien
27	273.5	45.2	355	2	AAW35133	Aaw35133 R. pipien
28	273.5	45.2	355	2	AAW35129	Aaw35129 R. pipien
29	273.5	45.2	366	2	AAW35132	Aaw35132 R. pipien
30	273.5	45.2	379	2	AAW35126	Aaw35126 R. pipien
31	272.5	45.0	104	2	AAW30302	Aaw30302 Recombina
32	272.5	45.0	104	2	AAY28870	Aay28870 Recombina
33	270.5	44.7	104	2	AAR12344	Aar12344 Protein w
34	270.5	44.7	104	2	AAR47303	Aar47303 ONCONASE
35	270.5	44.7	104	2	AAW00736	Aaw00736 Protein d
36	270.5	44.7	104	2	AAW14065	Aaw14065 Onconase
37	270.5	44.7	104	2	AAW06543	Aaw06543 Antitumou
38	270.5	44.7	104	2	AAW88233	Aaw88233 Rana pipi
39	270.5	44.7	104	2	AAY33322	Aay33322 Frog onco
40	268.5	44.4	105	2	AAW35116	Aaw35116 R. pipien
41	268.5	44.4	106	2	AAW35122	Aaw35122 R. pipien
42	268.5	44.4	107	2	AAW35117	Aaw35117 R. pipien
43	267.5	44.2	105	2	AAW35115	Aaw35115 R. pipien
44	264.5	43.7	358	2	AAW35127	Aaw35127 R. pipien
45	264.5	43.7	365	2	AAW35131	Aaw35131 R. pipien

ALIGNMENTS

RESULT 1
AAY28876
ID AAY28876 standard; protein; 111 AA.
XX
AC AAY28876;
XX
DT 25-JAN-2000 (first entry)
XX
DE Recombinant Met(-1) RaCOR1 Met22Leu Met57Leu-(His)6 protein.
XX
KW Met(-1) Rana catesbeiana ribonuclease Met22Leu Met57Leu-(His)6; RaCOR1;
KW recombinant; CD22; covalently bound; LL2 antibody; ligand binding moiety;
KW cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG;
KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
KW cancer; bullfrog; RNase; autoimmune disease.
XX
OS Rana catesbeiana.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1
FT /note= "Met not found in wild type RaCOR1"
FT Misc-difference 1
FT /note= "(His)6 histidine tag attached to N-terminal Met"
FT Misc-difference 23
FT /note= "Wild type Met replaced with Leu"
FT Misc-difference 58
FT /note= "Wild type Met replaced with Leu"
XX
PN WO9950398-A2.
XX
PD 07-OCT-1999.
XX
PF 26-MAR-1999; 99WO-US006641.
XX
PR 27-MAR-1998; 98US-0079751P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rybak SM, Newton DL;
XX
DR WPI; 1999-610847/52.
DR N-PSDB; AAZ08133.
XX
PT New recombinant ribonucleases, used for killing target cells, e.g. for
PT treating cancers, viral infections or autoimmune diseases.
XX
PS Claim 22; Page 66; 71pp; English.

```
RA   Beintema J.J.;
RT   "Secretory ribonuclease genes and pseudogenes in true ruminants.";
RL   Gene 212:259-268(1998).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y11670; CAA72368.1; -.
DR   HSSP; P00656; 1SRN.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT   ACT_SITE     41     41       BY SIMILARITY.
FT   DISULFID     26     84       BY SIMILARITY.
FT   DISULFID     40     95       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID     65     72       BY SIMILARITY.
FT   CARBOHYD     62     62       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   CARBOHYD    129    129       O-LINKED (BY SIMILARITY).
FT   CARBOHYD    133    133       O-LINKED (BY SIMILARITY).
SQ   SEQUENCE   151 AA;  16819 MW;  E95F3757FFC5B233 CRC64;

  Query Match             20.6%;  Score 123.5;  DB 1;  Length 151;
  Best Local Similarity   29.8%;  Pred. No. 2.2e-06;
  Matches   36;  Conservative   18;  Mismatches   44;  Indels   23;  Gaps    7;

Qy          4 ATFQQKHI------INTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINL 57
              | |:::|:           ||  ::     :  |:|| ||||:  |  :|||:|:
Db          6 AKFRRQHMDAGSSSSGNSNYCNQMMKRR-RMTHGRCKPVNTFVHESLDSVKAVCS---QK 61

Qy         58 NVL----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHFA 104
              |:          | :   :  |  |   :  | | | :  :  || | || | | ||||
Db         62 NITCKNGQPNCYQSNSTMNITDCRETGSSKYPNCAYKTSQKQKYITVACEGNPYVPVHFD 121

Qy        105 G 105
              |
Db        122 G 122


Search completed: May  7, 2004, 21:53:06
Job time : 5.55659 secs
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OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Milk, and Serum;
RX   MEDLINE=97409980; PubMed=9266695;
RA   Strydom D.J., Bond M.D., Vallee B.L.;
RT   "An angiogenic protein from bovine serum and milk -- purification and
RT   primary structure of angiogenin-2.";
RL   Eur. J. Biochem. 247:535-544(1997).
CC   -!- FUNCTION: Binds tightly to placental ribonuclease inhibitor and
CC       has very low ribonuclease activity. Has potent angiogenic
CC       activity. Angiogenin induces vascularization of normal and
CC       malignant tissues. Abolishes protein synthesis by specifically
CC       hydrolyzing cellular tRNAs.
CC   -!- TISSUE SPECIFICITY: Serum and milk.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR   HSSP; P10152; 1AGI.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Angiogenesis;
KW   Protein synthesis inhibitor; Glycoprotein;
KW   Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   ACT_SITE     12     12       BY SIMILARITY.
FT   ACT_SITE     39     39       BY SIMILARITY.
FT   ACT_SITE    113    113       BY SIMILARITY.
FT   DISULFID     25     80
FT   DISULFID     38     91
FT   DISULFID     56    106
FT   CARBOHYD     33     33       N-LINKED (GLCNAC. . .).
SQ   SEQUENCE   123 AA;  14522 MW;  B703B9839919FD2F CRC64;

  Query Match             20.6%;  Score 123.5;  DB 1;  Length 123;
  Best Local Similarity   29.6%;  Pred. No. 1.8e-06;
  Matches   32;  Conservative   20;  Mismatches   43;  Indels   13;  Gaps    5;

Qy          6 FQQKHIINTPI-----ICNTILDNNIYIVGGQCKRVNTFIISSATTVKAIC---TGVINL 57
              | :||   :|       |||:::     :   ||  ||||  ::  ::|:|    |
Db          8 FLRKHYDPSPTGHDDRYCNTMMERR--NMTRPCKDTNTFIHGNSDDIRAVCDDRNGEPYR 65

Qy         58 NVLSTTR--FQLNTCTRTSITPR-PCPYSSRTETNYICVKCENQYPVH 102
              | |  :|  ||: ||     :|| || | :       | ::| : :|:|
Db         66 NGLRRSRSPFQVTTCRHRGGSPRPPCRYRAFRANRVIVIRCRDGFPIH 113


RESULT 14
RNBR_GIRCA
ID   RNBR_GIRCA     STANDARD;      PRT;   141 AA.
AC   Q29542; Q29533;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ribonuclease, brain (EC 3.1.27.-) (BRB).
GN   BRN.
OS   Giraffa camelopardalis (Giraffe).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Giraffoidea;
OC   Giraffidae; Giraffa.
OX   NCBI_TaxID=9894;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96139017; PubMed=8587129;
RA   Confalone E., Beintema J.J., Sasso M.P., Carsana A., Palmieri M.,
RA   Vento M.T., Furia A.;
RT   "Molecular evolution of genes encoding ribonucleases in ruminant
RT   species.";
RL   J. Mol. Evol. 41:850-858(1995).
RN   [2]
RP   SEQUENCE OF 31-114 FROM N.A.
RX   MEDLINE=93367815; PubMed=8360916;
RA   Breukelman H.J., Beintema J.J., Confalone E., Costanzo C., Sasso M.P.,
RA   Carsana A., Palmieri M., Furia A.;
RT   "Sequences related to the ox pancreatic ribonuclease coding region in
RT   the genomic DNA of mammalian species.";
RL   J. Mol. Evol. 37:29-35(1993).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; S81743; AAB36137.1; -.
DR   EMBL; S65126; AAB27931.1; -.
DR   HSSP; P00656; 2RNS.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT   ACT_SITE     41     41       BY SIMILARITY.
FT   DISULFID     26     84       BY SIMILARITY.
FT   DISULFID     40     95       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID     65     72       BY SIMILARITY.
FT   CARBOHYD     62     62       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   CARBOHYD    129    129       O-LINKED (BY SIMILARITY).
SQ   SEQUENCE   141 AA;  15592 MW;  73745EFE9079591F CRC64;

  Query Match             20.6%;  Score 123.5;  DB 1;  Length 141;
  Best Local Similarity   29.8%;  Pred. No. 2.1e-06;
  Matches   36;  Conservative   18;  Mismatches   44;  Indels   23;  Gaps    7;

Qy          4 ATFQQKHI------INTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINL 57
              | |:::|:      :    || ::      :  |:|| ||||:  |   |||:|:
Db          6 AKFRRQHMDSGSSSSSNSNYCNQMMKRR-RMTHGRCKPVNTFVHESLADVKAVCS---QK 61

Qy         58 NVL----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHFA 104
              |:          | :   :  |  |   :  | | : :  :  || | || | | ||||
Db         62 NITCKNGQPNCYQSNSTMNITDCRETGSSKYPNCAYKTSQKQKYITVACEGNPYVPVHFD 121

Qy        105 G 105
              |
Db        122 G 122


RESULT 15
RNBR_AXIPR
ID   RNBR_AXIPR     STANDARD;      PRT;   151 AA.
AC   P87350;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Ribonuclease, brain (EC 3.1.27.-) (BRB).
GN   BRN.
OS   Axis porcinus (Hog deer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC   Cervidae; Cervinae; Axis.
OX   NCBI_TaxID=57737;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98278842; PubMed=9611269;
RA   Breukelman H.J., van der Munnik N., Kleineidam R.G., Furia A.,
```

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  Matches   37;  Conservative   18;  Mismatches   43;  Indels   23;  Gaps    7;

Qy          4 ATFQQKHI------INTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINL 57
              | |:::|:       : |  || ::     :  |:|| ||||:  |   |||:|:
Db         32 AKFRRQHMDSGSSSSSNPNYCNQMMKRR-RMTHGRCKPVNTFVHESLDDVKAVCS---QK 87

Qy         58 NVL----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHFA 104
              |:          | :   :  |  |  :  | | | :  :  || | || | | ||||
Db         88 NITCKNGHPNCYQSKSTMSITDCRETGSSKYPNCAYKTSQKQKYITVACEGNPYVPVHFD 147

Qy        105 G 105
              |
Db        148 G 148


RESULT 11
RNP_IGUIG
ID   RNP_IGUIG      STANDARD;      PRT;   119 AA.
AC   P80287;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
OS   Iguana iguana (Common iguana).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.
OX   NCBI_TaxID=8517;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Pancreas;
RX   MEDLINE=94139745; PubMed=8307028;
RA   Zhao W., Beintema J.J., Hofsteenge J.;
RT   "The amino acid sequence of iguana (Iguana iguana) pancreatic
RT   ribonuclease.";
RL   Eur. J. Biochem. 219:641-646(1994).
CC   -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC       phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC       with 2',3'-cyclic phosphate intermediates.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Pancreas.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR   PIR; S41111; S41111.
DR   HSSP; P00656; 1LSQ.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID     25     80       BY SIMILARITY.
FT   DISULFID     39     91       BY SIMILARITY.
FT   DISULFID     57    106       BY SIMILARITY.
FT   ACT_SITE     10     10       BY SIMILARITY.
FT   ACT_SITE     40     40       BY SIMILARITY.
FT   ACT_SITE    113    113       BY SIMILARITY.
SQ   SEQUENCE   119 AA;  13324 MW;  6072FB5B7B15BD5A CRC64;

  Query Match             21.2%;  Score 127.5;  DB 1;  Length 119;
  Best Local Similarity   29.6%;  Pred. No. 6.5e-07;
  Matches   34;  Conservative   17;  Mismatches   51;  Indels   13;  Gaps    4;

Qy          1 QNWATFQQKHI-------INTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAIC-- 51
              |:|::|| |||       |   |: ::     :   :||  |||: :| : :: :|
Db          1 QDWSSFQNKHIDYPETSASNPNAYCDLMMQRR-NLNPTKCKTRNTFVHASPSEIQQVCGS 59

Qy         52 --TGVINLNVLSTTRFQLNTCTRTSIT-PRPCPYSSRTETNYICVKCENQYPVHF 103
                |   :    |  | | |      | |  | |:    |  | : |||  ||||
Db         60 GGTHYEDNLYDSNESFDLTDCKNVGGTAPSSCKYNGTPGTKRIRIACENNQPVHF 114


RESULT 12
RNBR_CAPCA
ID   RNBR_CAPCA      STANDARD;      PRT;   151 AA.
AC   P79351;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Ribonuclease, brain (EC 3.1.27.-) (BRB).
OS   Capreolus capreolus (Roe deer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC   Cervidae; Odocoileinae; Capreolus.
OX   NCBI_TaxID=9858;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98278842; PubMed=9611269;
RA   Breukelman H.J., van der Munnik N., Kleineidam R.G., Furia A.,
RA   Beintema J.J.;
RT   "Secretory ribonuclease genes and pseudogenes in true ruminants.";
RL   Gene 212:259-268(1998).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; Y11673; CAA72371.1; -.
DR   HSSP; P00656; 1SRN.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT   ACT_SITE     41     41       BY SIMILARITY.
FT   DISULFID     26     84       BY SIMILARITY.
FT   DISULFID     40     95       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID     65     72       BY SIMILARITY.
FT   CARBOHYD     62     62       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   CARBOHYD    129    129       O-LINKED (BY SIMILARITY).
FT   CARBOHYD    133    133       O-LINKED (BY SIMILARITY).
SQ   SEQUENCE   151 AA;  16971 MW;  392D0E6302F006A6 CRC64;

  Query Match             20.8%;  Score 124.5;  DB 1;  Length 151;
  Best Local Similarity   28.6%;  Pred. No. 1.8e-06;
  Matches   34;  Conservative   18;  Mismatches   44;  Indels   23;  Gaps    6;

Qy          4 ATFQQKHI------INTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINL 57
              | |:::|:         |  || ::     :  |:|| ||||:  |   |||:|:
Db          6 AKFRRQHMDSGSSSSGNPNYCNQMMKRR-RMTHGRCKPVNTFVHESLDNVKAVCS---QK 61

Qy         58 NVL----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCENQ--YPVHF 103
              |:          | :   :  | :|  :  | | | :  :  || | ||     ||||
Db         62 NITCKNGQPNCYQSNSTMNITDCRQTGSSKYPNCAYKTSQKQKYITVACEGDPYVPVHF 120


RESULT 13
ANG2_BOVIN
ID   ANG2_BOVIN      STANDARD;      PRT;   123 AA.
AC   P80929;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Angiogenin-2 (EC 3.1.27.-).
GN   ANG2.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
GN   RNASE1 OR RNS1.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=70104197; PubMed=5460946;
RA   Jackson R.L., Hirs C.H.W.;
RT   "The primary structure of porcine pancreatic ribonuclease. II. The
RT   amino acid sequence of the reduced S-aminoethylated protein.";
RL   J. Biol. Chem. 245:637-653(1970).
RN   [2]
RP   REVISION TO 2.
RA   Wierenga R.K., Huizinga J.D., Gaastra W., Welling G.W., Beintema J.J.;
RT   "Affinity chromatography of porcine pancreatic ribonuclease and
RT   reinvestigation of the N-terminal amino acid sequence.";
RL   FEBS Lett. 31:181-185(1973).
RN   [3]
RP   DISULFIDE BONDS.
RX   MEDLINE=70104198; PubMed=4904878;
RA   Phelan J.J., Hirs C.H.W.;
RT   "The primary structure of porcine pancreatic ribonuclease. 3. The
RT   disulfide bonds.";
RL   J. Biol. Chem. 245:654-661(1970).
CC   -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC       phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC       with 2',3'-cyclic phosphate intermediates.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Pancreas.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR   PIR; A92071; NRPG.
DR   HSSP; P00656; 1SRN.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT   DISULFID     26     84
FT   DISULFID     40     95
FT   DISULFID     58    110
FT   DISULFID     65     72
FT   ACT_SITE     12     12       BY SIMILARITY.
FT   ACT_SITE     41     41       BY SIMILARITY.
FT   ACT_SITE    119    119       BY SIMILARITY.
FT   CARBOHYD     21     21       N-LINKED (GLCNAC. . .).
FT   CARBOHYD     34     34       N-LINKED (GLCNAC. . .).
FT   CARBOHYD     76     76       N-LINKED (GLCNAC. . .).
SQ   SEQUENCE   124 AA;  13804 MW;  0AC28CDE14111845 CRC64;

  Query Match             21.6%;  Score 129.5;  DB 1;  Length 124;
  Best Local Similarity   30.7%;  Pred. No. 4.1e-07;
  Matches   35;  Conservative   20;  Mismatches   42;  Indels   17;  Gaps    6;

Qy          6 FQQKHI------INTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGV-INLN 58
              ||::|:       |:   || ::     :  |:|| ||||:  |   |:|:|: : :|
Db          8 FQRQHMDPDSSSSNSSNYCNLMMSRR-NMTQGRCKPVNTFVHESLADVQAVCSQINVNCK 66

Qy         59 VLSTTRFQLNT------CTRTSITPRP-CPYSSRTETNYICVKCENQ--YPVHF 103
                 | :| |:      | :|  :  | | | :  |  :| | ||     ||||
Db         67 NGQTNCYQSNSTMHITDCRQTGSSKYPNCAYKASQEQKHIIVACEGNPPVPVHF 120


RESULT 10
RNBR_BOVIN
ID   RNBR_BOVIN     STANDARD;      PRT;   167 AA.
AC   P39873;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ribonuclease, brain precursor (EC 3.1.27.-) (BRB).
GN   BRN.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92093604; PubMed=1754384;
RA   Sasso M.P., Carsana A., Confalone E., Cosi C., Sorrentino S.,
RA   Viola M., Palmieri M., Russo E., Furia A.;
RT   "Molecular cloning of the gene encoding the bovine brain ribonuclease
RT   and its expression in different regions of the brain.";
RL   Nucleic Acids Res. 19:6469-6474(1991).
RN   [2]
RP   SEQUENCE OF 27-167, AND CARBOHYDRATE-LINKAGE SITES.
RC   TISSUE=Brain;
RX   MEDLINE=89214015; PubMed=3243767;
RA   Watanabe H., Katoh H., Ishii M., Komoda Y., Sanda A., Takizawa Y.,
RA   Ohgi K., Irie M.;
RT   "Primary structure of a ribonuclease from bovine brain.";
RL   J. Biochem. 104:939-945(1988).
RN   [3]
RP   SEQUENCE OF 27-167 FROM N.A.
RX   MEDLINE=96139017; PubMed=8587129;
RA   Confalone E., Beintema J.J., Sasso M.P., Carsana A., Palmieri M.,
RA   Vento M.T., Furia A.;
RT   "Molecular evolution of genes encoding ribonucleases in ruminant
RT   species.";
RL   J. Mol. Evol. 41:850-858(1995).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC   ----------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X59767; CAA42439.1; -.
DR   EMBL; S81744; AAB36138.1; -.
DR   PIR; S20066; S20066.
DR   HSSP; P00656; 2RNS.
DR   GlycoSuiteDB; P39873; -.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Glycoprotein; Signal.
FT   SIGNAL        1     26
FT   CHAIN        27    167       RIBONUCLEASE, BRAIN.
FT   ACT_SITE     38     38       BY SIMILARITY.
FT   ACT_SITE     67     67       BY SIMILARITY.
FT   ACT_SITE    145    145       BY SIMILARITY.
FT   DISULFID     52    110       BY SIMILARITY.
FT   DISULFID     66    121       BY SIMILARITY.
FT   DISULFID     84    136       BY SIMILARITY.
FT   DISULFID     91     98       BY SIMILARITY.
FT   CARBOHYD     88     88       N-LINKED (GLCNAC. . .).
FT                                /FTId=CAR_000005.
FT   CARBOHYD    155    155       O-LINKED.
FT   CARBOHYD    159    159       O-LINKED.
FT   CONFLICT    155    155       T -> S (IN REF. 2).
SQ   SEQUENCE   167 AA;  18450 MW;  681CAAC3CC2FC459 CRC64;

  Query Match             21.6%;  Score 129.5;  DB 1;  Length 167;
  Best Local Similarity   30.6%;  Pred. No. 5.7e-07;
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RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   PARTIAL SEQUENCE.
RC   TISSUE=Serum;
RX   MEDLINE=93192291; PubMed=8448182;
RA   Bond M.D., Strydom D.J., Vallee B.L.;
RT   "Characterization and sequencing of rabbit, pig and mouse
RT   angiogenins: discernment of functionally important residues and
RT   regions.";
RL   Biochim. Biophys. Acta 1162:177-186(1993).
CC   -!- FUNCTION: May function as a tRNA-specific ribonuclease that binds
CC       to actin on the surface of endothelial cells; once bound,
CC       angiogenin is endocytosed and translocated to the nucleus, thereby
CC       promoting the endothelial invasiveness necessary for blood vessel
CC       formation. Angiogenin induces vascularization of normal and
CC       malignant tissues. Abolishes protein synthesis by specifically
CC       hydrolyzing cellular tRNAs.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC   ----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U22516; AAA91366.1; -.
DR   EMBL; BC055355; AAH55355.1; -.
DR   PIR; A35932; A35932.
DR   HSSP; P03950; 1A4Y.
DR   MGD; MGI:88022; Ang.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Angiogenesis;
KW   Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
FT   SIGNAL        1     24
FT   CHAIN        25    145       ANGIOGENIN.
FT   MOD_RES      25     25       PYRROLIDONE CARBOXYLIC ACID (BY
FT                                SIMILARITY).
FT   ACT_SITE     37     37       BY SIMILARITY.
FT   ACT_SITE     64     64       BY SIMILARITY.
FT   ACT_SITE    137    137       BY SIMILARITY.
FT   DISULFID     50    104       BY SIMILARITY.
FT   DISULFID     63    115       BY SIMILARITY.
FT   DISULFID     81    130       BY SIMILARITY.
SQ   SEQUENCE   145 AA;  16228 MW;  06944260BB764938 CRC64;

  Query Match             22.8%;  Score 136.5;  DB 1;  Length 145;
  Best Local Similarity   40.3%;  Pred. No. 8.6e-08;
  Matches   31;  Conservative   11;  Mismatches   28;  Indels    7;  Gaps    3;

Qy         33 CKRVNTFIISSATTVKAICTG-----VINLNVLSTTRFQLNTCTRTSITPR-PCPYSSRT 86
              || |||||  : : :||||         ||  :| : ||: ||  |  :|| || | :
Db         63 CKDVNTFIHGNKSNIKAICGANGSPYRENLR-MSKSPFQVTTCKHTGGSPRPPCQYRASA 121

Qy         87 ETNYICVKCENQYPVHF 103
              :: : |||  ||||
Db        122 GFRHVVIACENGLPVHF 138


RESULT 8
RNP_BALAC
ID   RNP_BALAC      STANDARD;      PRT;   124 AA.
AC   P00673;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
GN   RNASE1 OR RNS1.
OS   Balaenoptera acutorostrata (Minke whale) (Lesser rorqual).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
OC   Balaenopteridae; Balaenoptera.
OX   NCBI_TaxID=9767;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76277855; PubMed=962870;
RA   Emmens M., Welling G.W., Beintema J.J.;
RT   "The amino acid sequence of pike-whale (lesser-rorqual) pancreatic
RT   ribonuclease.";
RL   Biochem. J. 157:317-323(1976).
CC   -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC       phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC       with 2',3'-cyclic phosphate intermediates.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Pancreas.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR   PIR; A00818; NRWHK.
DR   HSSP; P00656; 1SRN.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT   DISULFID     26     84       BY SIMILARITY.
FT   DISULFID     40     95       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID     65     72       BY SIMILARITY.
FT   ACT_SITE     12     12       BY SIMILARITY.
FT   ACT_SITE     41     41       BY SIMILARITY.
FT   ACT_SITE    119    119       BY SIMILARITY.
FT   CARBOHYD     76     76       N-LINKED (GLCNAC. . .) (30%).
SQ   SEQUENCE   124 AA;  14125 MW;  F57475459F697E20 CRC64;

  Query Match             21.9%;  Score 131.5;  DB 1;  Length 124;
  Best Local Similarity   32.5%;  Pred. No. 2.5e-07;
  Matches   38;  Conservative   17;  Mismatches   39;  Indels   23;  Gaps    7;

Qy          6 FQQKHII------NTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 59
              ||::|:        | |  || ::     :  |:|| ||||:  |   |||:|:     ||
Db          8 FQRQHMDSGNSPGNNPNYCNQMMMRR-KMTQGRCKPVNTFVHESLEDVKAVCS---QKNV 63

Qy         60 L----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 103
              |          | :   :  | :|  :  | | | :  :  :| | || | | ||||
Db         64 LCKNGRTNCYESNSTMHITDCRQTGSSKYPNCAYKTSQKEKHIIVACEGNPYVPVHF 120


RESULT 9
RNP_PIG
ID   RNP_PIG        STANDARD;      PRT;   124 AA.
AC   P00671;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
```

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RT   developmentally regulated genes when expressed in NIH 3T3
RT   fibroblasts.";
RL   Mol. Cell. Biol. 17:1503-1512(1997).
CC   -!- FUNCTION: Angiogenin induces vascularization of normal and
CC       malignant tissues. Abolishes protein synthesis by specifically
CC       hydrolyzing cellular tRNAs (By similarity).
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U72672; AAC05794.1; -.
DR   HSSP; P10152; 1AGI.
DR   MGD; MGI:1201793; Angl.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Angiogenesis;
KW   Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
FT   SIGNAL        1     24       POTENTIAL.
FT   CHAIN        25    145       ANGIOGENIN-3.
FT   MOD_RES      25     25       PYRROLIDONE CARBOXYLIC ACID
FT                                (BY SIMILARITY).
FT   ACT_SITE     37     37       BY SIMILARITY.
FT   ACT_SITE     64     64       BY SIMILARITY.
FT   ACT_SITE    137    137       BY SIMILARITY.
FT   DISULFID     50    104       BY SIMILARITY.
FT   DISULFID     63    115       BY SIMILARITY.
FT   DISULFID     81    130       BY SIMILARITY.
SQ   SEQUENCE   145 AA;  16696 MW;  DE9D3BC92F1D682C CRC64;

  Query Match             25.8%;  Score 154.5;  DB 1;  Length 145;
  Best Local Similarity   43.6%;  Pred. No. 9.9e-10;
  Matches   34;  Conservative   12;  Mismatches   23;  Indels    9;  Gaps    4;

Qy         33 CKRVNTFIISSATTVKAIC------TGVINLNVLSTTRFQLNTCTRTSITPR-PCPYSSR 85
              || |||||  :   :||||       || |  : | :|||: |||    :|| || |::
Db         63 CKEVNTFIHDTKNNIKAICGENGRPYGV-NFRI-SNSRFQVTTCTHKGGSPRPPCQYNAF 120

Qy         86 TETNYICVKCENQYPVHF 103
                :  || : ||: :||||
Db        121 KDFRYIVIACEDGWPVHF 138


RESULT 6
ANGR_MOUSE
ID   ANGR_MOUSE     STANDARD;      PRT;   145 AA.
AC   Q64438;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Angiogenin-related protein precursor.
GN   ANGRP.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129; TISSUE=Liver;
RX   MEDLINE=96079109; PubMed=8530072;
RA   Brown W.E., Nobile V., Subramanian V., Shapiro R.;
RT   "The mouse angiogenin gene family: structures of an angiogenin-related
RT   protein gene and two pseudogenes.";
RL   Genomics 29:200-206(1995).
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U22519; AAA91367.1; -.
DR   HSSP; P03950; 1A4Y.
DR   MGD; MGI:104984; Angrp.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal; Hydrolase; Nuclease; Endonuclease;
KW   Pyrrolidone carboxylic acid.
FT   SIGNAL        1     24       POTENTIAL.
FT   CHAIN        25    145       ANGIOGENIN-RELATED PROTEIN.
FT   MOD_RES      25     25       PYRROLIDONE CARBOXYLIC ACID (BY
FT                                SIMILARITY).
FT   ACT_SITE     37     37       BY SIMILARITY.
FT   ACT_SITE     64     64       BY SIMILARITY.
FT   ACT_SITE    137    137       BY SIMILARITY.
FT   DISULFID     50    104       BY SIMILARITY.
FT   DISULFID     63    115       BY SIMILARITY.
FT   DISULFID     81    130       BY SIMILARITY.
SQ   SEQUENCE   145 AA;  16612 MW;  29A6EB814429C4AD CRC64;

  Query Match             24.9%;  Score 149.5;  DB 1;  Length 145;
  Best Local Similarity   44.2%;  Pred. No. 3.4e-09;
  Matches   34;  Conservative    9;  Mismatches   27;  Indels    7;  Gaps    3;

Qy         33 CKRVNTFIISSATTVKAICTGV-----INLNVLSTTRFQLNTCTRTSITPR-PCPYSSRT 86
              || |||||  :   :||||       || : | :|||: |||    :|| || | :
Db         63 CKDVNTFIHDTKNNIKAICGKKGSPYGRNLRI-SKSRFQVTTCTHKGRSPRPPCRYRASK 121

Qy         87 ETNYICVKCENQYPVHF 103
                || : ||| :||||
Db        122 GFRYIIIGCENGWPVHF 138


RESULT 7
ANGI_MOUSE
ID   ANGI_MOUSE     STANDARD;      PRT;   145 AA.
AC   P21570;
DT   01-MAY-1991 (Rel. 18, Created)
DT   01-MAY-1991 (Rel. 18, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).
GN   ANG.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91025023; PubMed=2222458;
RA   Bond M.D., Vallee B.L.;
RT   "Isolation and sequencing of mouse angiogenin DNA.";
RL   Biochem. Biophys. Res. Commun. 171:988-995(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Liver;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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RL   J. Biochem. 106:729-735(1989).
CC   -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC       phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC       with 2',3'-cyclic phosphate intermediates.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR   PIR; JX0085; JX0085.
DR   HSSP; P11916; 1BC4.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   ACT_SITE     10     10       BY SIMILARITY.
FT   ACT_SITE     35     35       BY SIMILARITY.
FT   ACT_SITE    104    104       BY SIMILARITY.
FT   DISULFID     19     72       BY SIMILARITY.
FT   DISULFID     34     82       BY SIMILARITY.
FT   DISULFID     52     97       BY SIMILARITY.
FT   DISULFID     94    111       PROBABLE.
SQ   SEQUENCE   111 AA;  12461 MW;  D64BA72456C10788 CRC64;

  Query Match             61.7%;  Score 370;  DB 1;  Length 111;
  Best Local Similarity   64.9%;  Pred. No. 4.7e-33;
  Matches   72;  Conservative   10;  Mismatches   27;  Indels    2;  Gaps    2;

Qy          1 QNWATFQQKHIINTPII-CNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58
              |||| |::||| :|  | ||||:|  |||||:||  |||||||   |||||:||  :
Db          1 QNWAKFKEKHIRSTSSIDCNTIMDKAIYIVGGKCKERNTFIISSEDNVKAICSGVSPDRK 60

Qy         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              |||| |:|||| | ||||||||    : | |||||| | |||| |||:|
Db         61 ELSTTSFKLNTCIRDSITPRPCPYHPSPDNNKICVKCEKQLPVHFVGIGKC 111


RESULT 4
RN30_RANPI
ID   RN30_RANPI     STANDARD;      PRT;   104 AA.
AC   P22069;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   P-30 protein (EC 3.1.27.-) (Onconase).
OS   Rana pipiens (Northern leopard frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8404;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Embryo;
RX   MEDLINE=91093131; PubMed=1985896;
RA   Ardelt W., Mikulski S.M., Shogen K.;
RT   "Amino acid sequence of an anti-tumor protein from Rana pipiens
RT   oocytes and early embryos. Homology to pancreatic ribonucleases.";
RL   J. Biol. Chem. 266:245-251(1991).
RN   [2]
RP   3D-STRUCTURE MODELING.
RX   MEDLINE=93066156; PubMed=1438177;
RA   Mosimann S.C., Johns K.L., Ardelt W., Mikulski S.M., Shogen K.,
RA   James M.N.G.;
RT   "Comparative molecular modeling and crystallization of P-30 protein:
RT   a novel antitumor protein of Rana pipiens oocytes and early
RT   embryos.";
RL   Proteins 14:392-400(1992).
RN   [3]
RP   X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
RX   MEDLINE=94166079; PubMed=8120892;
RA   Mosimann S.C., Ardelt W., James M.N.G.;
RT   "Refined 1.7 A X-ray crystallographic structure of P-30 protein, an
RT   amphibian ribonuclease with anti-tumor activity.";
RL   J. Mol. Biol. 236:1141-1153(1994).
CC   -!- FUNCTION: Basic protein with antiproliferative/cytotoxic activity
CC       against several tumor cell lines in vitro, as well as antitumor
CC       in vivo. It exhibits a ribonuclease-like activity against high
CC       molecular weight ribosomal RNA.
CC   -!- DEVELOPMENTAL STAGE: Early embryos (up to four blastomere stage).
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR   PDB; 1ONC; 31-JAN-94.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; 3D-structure;
KW   Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   ACT_SITE     10     10
FT   ACT_SITE     31     31
FT   ACT_SITE     97     97
FT   DISULFID     19     68
FT   DISULFID     30     75
FT   DISULFID     48     90
FT   DISULFID     87    104
FT   HELIX         3     10
FT   STRAND       11     12
FT   HELIX        19     22
FT   TURN         23     24
FT   TURN         26     30
FT   STRAND       33     38
FT   HELIX        41     45
FT   HELIX        46     48
FT   TURN         49     50
FT   STRAND       55     58
FT   STRAND       63     70
FT   TURN         74     75
FT   STRAND       77     84
FT   STRAND       86     91
FT   TURN         92     93
FT   STRAND       94    101
SQ   SEQUENCE   104 AA;  11845 MW;  22A753C2F9E566B4 CRC64;

  Query Match             45.6%;  Score 273.5;  DB 1;  Length 104;
  Best Local Similarity   48.6%;  Pred. No. 1.1e-22;
  Matches   54;  Conservative   16;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          1 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58
              |:| |||:||| ||  : |: |:  |::     ||  |||| |    ||||| |:| : |
Db          1 QDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56

Qy         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104


RESULT 5
ANG3_MOUSE
ID   ANG3_MOUSE     STANDARD;      PRT;   145 AA.
AC   P97802;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Angiogenin-3 precursor (EC 3.1.27.-) (Angiogenin-related protein 2)
DE   (EF-5).
GN   ANG3 OR ANGL.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RX   MEDLINE=97184476; PubMed=9032278;
RA   Fu X., Kamps M.P.;
RT   "E2a-Pbx1 induces aberrant expression of tissue-specific and
```

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CC       residues with a 3'flanking guanine. Hydrolyzes poly(U) and poly(C)
CC       as substrates, and prefers the former. The S-lectins in frog eggs
CC       may be involved in the fertilization and development of the frog
CC       embryo. This lectin agglutinates various animal cells, including
CC       normal lymphocytes, erythrocytes, and fibroblasts of animal and
CC       human origin. It is cytotoxic against several tumor cells.
CC   -!- SUBUNIT: Monomer.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF039104; AAD10702.1; -.
DR   PIR; A27121; A27121.
DR   PDB; 1BC4; 28-OCT-98.
DR   PDB; 1M07; 21-JAN-03.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure;
KW   Signal; Pyrrolidone carboxylic acid.
FT   SIGNAL        1     22
FT   CHAIN        23    133       RIBONUCLEASE, OOCYTES.
FT   MOD_RES      23     23       PYRROLIDONE CARBOXYLIC ACID.
FT   ACT_SITE     32     32
FT   ACT_SITE     57     57
FT   ACT_SITE    125    125
FT   DISULFID     41     93
FT   DISULFID     56    103
FT   DISULFID     74    118
FT   DISULFID    115    132
FT   HELIX        25     32
FT   HELIX        41     45
FT   TURN         48     49
FT   STRAND       59     63
FT   HELIX        67     73
FT   TURN         74     74
FT   STRAND       79     84
FT   STRAND       90     95
FT   STRAND      105    110
FT   STRAND      114    119
FT   TURN        120    121
FT   STRAND      122    129
SQ   SEQUENCE   133 AA;  14762 MW;  A7D62594F7D16F0C CRC64;

  Query Match             97.6%;  Score 585.5;  DB 1;  Length 133;
  Best Local Similarity   97.3%;  Pred. No. 3.6e-56;
  Matches  108;  Conservative    2;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 QNWATFQQKHIINTPII-CNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 59
              |||||||||||||||| |||:|||||||||||||||||||||||||||||||||:||
Db         23 QNWATFQQKHIINTPIINCNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 82

Qy         60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 133


RESULT 2
LECS_RANJA
ID   LECS_RANJA     STANDARD;      PRT;   111 AA.
AC   P18839;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Sialic acid-binding lectin (EC 3.1.27.-).
OS   Rana japonica (Japanese reddish frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8402;
RN   [1]
RP   SEQUENCE, AND DISULFIDE BONDS.
RC   TISSUE=Egg;
RX   MEDLINE=91035319; PubMed=2229005;
RA   Kamiya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawauchi H.,
RA   Takayanagi Y., Titani K.;
RT   "Amino acid sequence of a lectin from Japanese frog (Rana japonica)
RT   eggs.";
RL   J. Biochem. 108:139-143(1990).
CC   -!- FUNCTION: The S-lectins in frog eggs may be involved in the
CC       fertilization and development of the frog embryo. This lectin
CC       preferentially agglutinate a large variety of tumor cells, but it
CC       does not agglutinate non-transformed cells and erythrocytes.
CC   -!- SUBUNIT: Monomer.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR   PIR; JX0120; JX0120.
DR   HSSP; P11916; 1BC4.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin;
KW   Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   ACT_SITE     10     10       BY SIMILARITY.
FT   ACT_SITE     35     35       BY SIMILARITY.
FT   ACT_SITE    104    104       BY SIMILARITY.
FT   DISULFID     19     72
FT   DISULFID     34     82
FT   DISULFID     52     97
FT   DISULFID     94    111
SQ   SEQUENCE   111 AA;  12326 MW;  FDEBDDF3834ED679 CRC64;

  Query Match             75.2%;  Score 451;  DB 1;  Length 111;
  Best Local Similarity   77.5%;  Pred. No. 9e-42;
  Matches   86;  Conservative    8;  Mismatches   15;  Indels    2;  Gaps    2;

Qy          1 QNWATFQQKHIINTP-IICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGV-INLN 58
              |||| ||:||| ||  | ||||:| :|||||||||  |||||||||||||||:|   | |
Db          1 QNWAKFQEKHIPNTSNINCNTIMDKSIYIVGGQCKERNTFIISSATTVKAICSGASTNRN 60

Qy         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              |||||||||||| |::  |||||||:|||||| |||||||: ||||||||||
Db         61 VLSTTRFQLNTCIRSATAPRPCPYNSRTETNVICVKCENRLPVHFAGIGRC 111


RESULT 3
RNPL_RANCA
ID   RNPL_RANCA     STANDARD;      PRT;   111 AA.
AC   P14626;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Ribonuclease, liver (EC 3.1.27.5).
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Liver;
RX   MEDLINE=90130374; PubMed=2613682;
RA   Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,
RA   Okazaki T., Ohgi K., Irie M.;
RT   "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana)
RT   liver.";
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 7, 2004, 21:30:40 ; Search time 5.55659 Seconds
(without alignments)
1030.796 Million cell updates/sec

Title: US-09-961-400-19
Perfect score: 600
Sequence: 1 QNWATFQQKHIINTPIICNT.....ICVKCENQYPVHFAGIGRCP 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	585.5	97.6	133	1	RNPO_RANCA	P11916 rana catesb
2	451	75.2	111	1	LECS_RANJA	P18839 rana japoni
3	370	61.7	111	1	RNPL_RANCA	P14626 rana catesb
4	273.5	45.6	104	1	RN30_RANPI	P22069 rana pipien
5	154.5	25.8	145	1	ANG3_MOUSE	P97802 mus musculu
6	149.5	24.9	145	1	ANGR_MOUSE	Q64438 mus musculu
7	136.5	22.8	145	1	ANGI_MOUSE	P21570 mus musculu
8	131.5	21.9	124	1	RNP_BALAC	P00673 balaenopter
9	129.5	21.6	124	1	RNP_PIG	P00671 sus scrofa
10	129.5	21.6	167	1	RNBR_BOVIN	P39873 bos taurus
11	127.5	21.2	119	1	RNP_IGUIG	P80287 iguana igua
12	124.5	20.8	151	1	RNBR_CAPCA	P79351 capreolus c
13	123.5	20.6	123	1	ANG2_BOVIN	P80929 bos taurus
14	123.5	20.6	141	1	RNBR_GIRCA	Q29542 giraffa cam
15	123.5	20.6	151	1	RNBR_AXIPR	P87350 axis porcin
16	123	20.5	146	1	ANGI_MIOTA	Q8wn65 miopithecus
17	123	20.5	146	1	ANGI_SAISC	Q8wn60 saimiri sci
18	120	20.0	146	1	ANGI_CERAE	Q8wn66 cercopithec
19	120	20.0	147	1	ANGI_PONPY	Q8wn67 pongo pygma
20	119.5	19.9	143	1	RNBR_SHEEP	Q29543 ovis aries
21	119	19.8	122	1	RNP_MACRU	P00686 macropus ru
22	118.5	19.8	123	1	ANGI_PIG	P31346 sus scrofa
23	118.5	19.8	124	1	RNP_ANTAM	P00668 antilocapra
24	118	19.7	146	1	ANGI_AOTTR	Q8wn61 aotus trivi
25	117	19.5	146	1	ANGI_SAGOE	Q8wn62 saguinus oe
26	116.5	19.4	128	1	RNP_MYOCO	P00676 myocastor c
27	116.5	19.4	149	1	RNP_MOUSE	P00683 mus musculu
28	115	19.2	146	1	ANGI_MACMU	Q8wn63 macaca mula
29	114.5	19.1	128	1	RNPB_CAVPO	P00679 cavia porce
30	114	19.0	148	1	ANGI_BOVIN	P10152 bos taurus
31	113.5	18.9	124	1	RNP_CAMDR	P00670 camelus dro
32	113.5	18.9	128	1	RNP_HORSE	P00674 equus cabal
33	113	18.8	147	1	ANGI_HUMAN	P03950 homo sapien
34	113	18.8	147	1	ANGI_PANTR	Q8wme8 pan troglod
35	112.5	18.8	119	1	RNS4_BOVIN	P15467 bos taurus
36	112.5	18.8	128	1	RNP_PROGU	P04059 proechimys
37	109.5	18.2	124	1	RNP_RANTA	P00666 rangifer ta
38	109.5	18.2	146	1	ANGI_PAPHA	Q8wn64 papio hamad
39	109.5	18.2	148	1	RNS4_MOUSE	Q9jjh1 mus musculu
40	109	18.2	125	1	ANGI_RABIT	P31347 oryctolagus
41	108.5	18.1	124	1	RNP_CAPCA	P00664 capreolus c
42	108.5	18.1	124	1	RNP_GIRCA	P00662 giraffa cam
43	108.5	18.1	130	1	RNP_CRILO	P24717 cricetulus
44	107.5	17.9	124	1	RNP_BUBBU	P00657 bubalus bub
45	107.5	17.9	148	1	RNP_PERLE	Q9wuv5 peromyscus

ALIGNMENTS

RESULT 1
RNPO_RANCA
ID RNPO_RANCA STANDARD; PRT; 133 AA.
AC P11916; Q9PWR7;
DT 01-OCT-1989 (Rel. 12, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ribonuclease, oocytes precursor (EC 3.1.27.-) (RC-RNase) (Sialic acid-
DE binding lectin) (SBL-C).
GN RCR.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98165825; PubMed=9497370;
RA Huang H.C., Wang S.C., Leu Y.J., Lu S.C., Liao Y.D.;
RT "The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease.
RT Tissue distribution, cloning, purification, cytotoxicity, and active
RT residues for RNase activity.";
RL J. Biol. Chem. 273:6395-6401(1998).
RN [2]
RP SEQUENCE OF 23-133.
RC TISSUE=Egg;
RX MEDLINE=87299649; PubMed=3304421;
RA Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H.,
RA Takayanagi G., Hakomori S.;
RT "Amino acid sequence of sialic acid binding lectin from frog (Rana
RT catesbeiana) eggs.";
RL Biochemistry 26:2189-2194(1987).
RN [3]
RP CHARACTERIZATION, AND SEQUENCE OF 81-101.
RX MEDLINE=92220613; PubMed=1373237;
RA Liao Y.-D.;
RT "A pyrimidine-guanine sequence-specific ribonuclease from Rana
RT catesbeiana (bullfrog) oocytes.";
RL Nucleic Acids Res. 20:1371-1377(1992).
RN [4]
RP CHARACTERIZATION.
RC TISSUE=Egg;
RX MEDLINE=93192604; PubMed=8448385;
RA Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawauchi H.,
RA Takayanagi Y., Hakomori S., Titani K.;
RT "Ribonuclease activity of sialic acid-binding lectin from Rana
RT catesbeiana eggs.";
RL Glycobiology 3:37-45(1993).
RN [5]
RP STRUCTURE BY NMR OF 23-133.
RX MEDLINE=98437383; PubMed=9761686;
RA Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;
RT "The solution structure of a cytotoxic ribonuclease from the oocytes
RT of Rana catesbeiana (bullfrog).";
RL J. Mol. Biol. 283:231-244(1998).
CC -!- FUNCTION: Preferentially cleaves single-stranded RNA at pyrimidine

```
Qy          6 FQQKHI------INTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 59
              ||::|:      ||:|  || ::     :  | || ||||:      |:|:|:      ||
Db         33 FQRQHMDPDGSSINSPTYCNQMMKRR-DMTNGSCKPVNTFVHEPLADVQAVCS---QENV 88

Qy         60 L----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 103
                        |::   :  |     :  | | | :     :| | || | | ||||
Db         89 TCKNRKSNCYKSSSALHITDCHLKGNSKYPNCDYKTTQYQKHIIVACEGNPYVPVHF 145


RESULT 15
NRGPB
pancreatic ribonuclease (EC 3.1.27.5) B - guinea pig (tentative sequence)
N;Alternate names: RNase IB
C;Species: Cavia porcellus (guinea pig)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C;Accession: A00826
R;van den Berg, A.; van den Hende-Timmer, L.; Hofsteenge, J.; Gaastra, W.; Beintema, J.J
Eur. J. Biochem. 75, 91-100, 1977
A;Title: Guinea pig pancreatic ribonucleases. Isolation, properties, primary structure a
A;Reference number: A91247; MUID:77185023; PMID:862624
A;Accession: A00826
A;Molecule type: protein
A;Residues: 1-128 <VAN>
A;Note: 64-Pro was also found
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;21,34/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted

  Query Match             19.1%;  Score 114.5;  DB 1;  Length 128;
  Best Local Similarity   30.8%;  Pred. No. 0.00024;
  Matches   36;  Conservative   15;  Mismatches   43;  Indels   23;  Gaps    6;

Qy          6 FQQKHI------INTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 59
              ||::|:       |:   || ::     :  |:|| ||||:  |   |:|:|      ||
Db          8 FQRQHMDPEGSPSNSSNYCNVMMIRR-NMTQGRCKPVNTFVHESLADVQAVC---FQKNV 63

Qy         60 L----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCENQ--YPVHF 103
              |          | :| ::  |  || :  | | |        | | ||     ||||
Db         64 LCKNGQTNCYQSYSRMRITDCRVTSSSKFPNCSYRMSQAQKSIIVACEGDPYVPVHF 120


Search completed: May  7, 2004, 21:54:56
Job time : 10.9813 secs
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Db          7 FQRQHMDTEHSTASSSNYCNLMMKAR-DMTSGRCKPLNTFIHEPKSVVDAVCHQENVTCK 65

Qy         52 TGVINLNVLSTTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCENQY-PVHF 103

Db         66 NGRTNC-YKSNSRLSITNCRQTGASKYPNCQYETSNLNKQIIVACEGQYVPVHF 118


RESULT 11
A43825
angiogenin - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S29834; A43825
R;Bond, M.D.; Strydom, D.J.; Vallee, B.L.
Biochim. Biophys. Acta 1162, 177-186, 1993
A;Title: Characterization and sequencing of rabbit, pig and mouse angiogenins: discernme
A;Reference number: S29833; MUID:93192291; PMID:8448182
A;Accession: S29834
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-123 <BON>
A;Note: this sequence was submitted to the Protein Sequence Database, December 1992
C;Superfamily: pancreatic ribonuclease

  Query Match             19.8%;  Score 118.5;  DB 1;  Length 123;
  Best Local Similarity   39.5%;  Pred. No. 9.3e-05;
  Matches   30;  Conservative    6;  Mismatches   35;  Indels    5;  Gaps    2;

Qy         33 CKRVNTFIISSATTVKAICTG----VINLNVLSTTRFQLNTCTRTSITPR-PCPYSSRTE 87

Db         39 CKEVNTFIHGTRNDIKAICNDKNGEPYNNFRRSKSPFQITTCKHKGGSNRPPCGYRATAG 98

Qy         88 TNYICVKCENQYPVHF 103

Db         99 FRTIAVACENGLPVHF 114


RESULT 12
NRPRH
pancreatic ribonuclease (EC 3.1.27.5) - pronghorn (tentative sequence)
N;Alternate names: RNase 1; RNase A
C;Species: Antilocapra americana (pronghorn)
C;Date: 28-Feb-1981 #sequence_revision 28-Feb-1981 #text_change 31-Mar-2000
C;Accession: A00813
R;Beintema, J.J.; Gaastra, W.; Munniksma, J.
J. Mol. Evol. 13, 305-316, 1979
A;Title: Primary structure of pronghorn pancreatic ribonuclease: close relationship betw
A;Reference number: A00813; MUID:80075014; PMID:513141
A;Accession: A00813
A;Molecule type: protein
A;Residues: 1-124 <BEI>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F;34/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

  Query Match             19.8%;  Score 118.5;  DB 1;  Length 124;
  Best Local Similarity   29.9%;  Pred. No. 9.3e-05;
  Matches   35;  Conservative   19;  Mismatches   44;  Indels   19;  Gaps    7;

Qy          4 ATFQQKHIINTPI------ICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICT----- 52

Db          6 AKFERQHIDSNPSSVSSSNYCNQMMKSR-NLTQGRCKPVNTFVHESLADVQAVCSQKNVA 64

Qy         53 ---GVINLNVLSTTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 103

Db         65 CKNGQTNC-YQSYSTMSITDCRETGSSKYPNCAYKTTQAKKHIIVACEGNPYVPVHY 120


RESULT 13
NRCU
pancreatic ribonuclease (EC 3.1.27.5) - nutria (tentative sequence)
N;Alternate names: RNase 1; RNase A
C;Species: Myocastor coypus (nutria, coypu)
C;Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
C;Accession: A00822
R;van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
Biochim. Biophys. Acta 453, 400-409, 1976
A;Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic r
A;Reference number: A90612; MUID:77065676; PMID:999896
A;Accession: A00822
A;Molecule type: protein
A;Residues: 1-128 <VAN>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F;34/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match             19.4%;  Score 116.5;  DB 1;  Length 128;
  Best Local Similarity   30.8%;  Pred. No. 0.00015;
  Matches   36;  Conservative   16;  Mismatches   42;  Indels   23;  Gaps    7;

Qy          6 FQQKHI------INTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 59

Db          8 FERQHMDSRGSPSTNPNYCNEMMKSR-NMTQGRCKPVNTFVHEPLADVQAVC---FQKNV 63

Qy         60 L----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 103

Db         64 LCKNGQTNCYQSNSNMHITDCRVTSNSDYPNCSYRTSQEEKSIVVACEGNPYVPVHF 120


RESULT 14
NRMS
pancreatic ribonuclease (EC 3.1.27.5) precursor - mouse
N;Alternate names: RNase 1; RNase A
C;Species: Mus musculus (house mouse)
C;Date: 30-Nov-1980 #sequence_revision 13-Mar-1997 #text_change 18-Jun-1999
C;Accession: A34090; S22598; A00830
R;Schueller, C.; Nijssen, H.M.J.; Kok, R.; Beintema, J.J.
Mol. Biol. Evol. 7, 29-44, 1990
A;Title: Evolution of nucleic acids coding for ribonucleases: the mRNA sequence of mouse
A;Reference number: A34090; MUID:90136034; PMID:2299980
A;Accession: A34090
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-149 <SCH>
A;Cross-references: GB:M27814; NID:g200762; PIDN:AAA40060.1; PID:g200763
R;Samuelson, L.C.; Wiebauer, K.; Howard, G.; Schmid, R.M.; Koeplin, D.; Meisler, M.H.
Nucleic Acids Res. 19, 6935-6941, 1991
A;Title: Isolation of the murine ribonuclease gene Rib-1: structure and tissue specific e
A;Reference number: S22598; MUID:92107684; PMID:1840677
A;Accession: S22598
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-149 <SAM>
A;Cross-references: EMBL:X60103; NID:g53981; PIDN:CAA42697.1; PID:g53982
R;Lenstra, J.A.; Beintema, J.J.
Eur. J. Biochem. 98, 399-408, 1979
A;Title: The amino acid sequence of mouse pancreatic ribonuclease.
A;Reference number: A00830; MUID:80024269; PMID:556267
A;Accession: A00830
A;Molecule type: protein
A;Residues: 26-149 <LEN>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-149/Product: pancreatic ribonuclease #status experimental <MAT>
F;37,66,144/Active site: His, Lys, His #status predicted
F;51-109,65-120,83-135,90-97/Disulfide bonds: #status predicted
F;62,87/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             19.4%;  Score 116.5;  DB 1;  Length 149;
  Best Local Similarity   29.9%;  Pred. No. 0.00018;
  Matches   35;  Conservative   17;  Mismatches   42;  Indels   23;  Gaps    7;
```

NRPG
pancreatic ribonuclease (EC 3.1.27.5) - pig
N;Alternate names: RNase 1; RNase A
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
C;Accession: A92071; A91391; A00816
R;Jackson, R.L.; Hirs, C.H.W.
J. Biol. Chem. 245, 637-653, 1970
A;Title: The primary structure of porcine pancreatic ribonuclease. II. The amino acid se
A;Reference number: A92071; MUID:70104197; PMID:5460946
A;Accession: A92071
A;Molecule type: protein
A;Residues: 1,'Q',3-124 <JAC>
R;Wierenga, R.K.; Huizinga, J.D.; Gaastra, W.; Welling, G.W.; Beintema, J.J.
FEBS Lett. 31, 181-185, 1973
A;Title: Affinity chromatography of porcine pancreatic ribonuclease and reinvestigation
A;Reference number: A91391
A;Accession: A91391
A;Molecule type: protein
A;Residues: 1-124 <WIE>
R;Phelan, J.J.; Hirs, C.H.W.
J. Biol. Chem. 245, 654-661, 1970
A;Title: The primary structure of porcine pancreatic ribonuclease. III. The disulfide bo
A;Reference number: A92072; MUID:70104198; PMID:4904878
A;Contents: annotation; disulfide bonds
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;21,34,76/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status experimental

Query Match 21.6%; Score 129.5; DB 1; Length 124;
Best Local Similarity 30.7%; Pred. No. 7.6e-06;
Matches 35; Conservative 20; Mismatches 42; Indels 17; Gaps 6;

```
Qy          6 FQQKHI------INTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGV-INLN 58
              ||::|:       |:   || ::     :  |:|| ||||:  |   |:|:|: : :|
Db          8 FQRQHMDPDSSSSNSSNYCNLMMSRR-NMTQGRCKPVNTFVHESLADVQAVCSQINVNCK 66

Qy         59 VLSTTRFQLNT------CTRTSITPRP-CPYSSRTETNYICVKCENQ--YPVHF 103
                |  :| |:      | :|  :  | | | :  |  :| | ||     ||||
Db         67 NGQTNCYQSNSTMHITDCRQTGSSKYPNCAYKASQEQKHIIVACEGNPPVPVHF 120
```

RESULT 8
S20066
pancreatic-type ribonuclease (EC 3.1.27.5) BRb precursor, brain - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 22-Nov-1993 #sequence_revision 12-May-1995 #text_change 22-Jun-1999
C;Accession: S20066; JX0056
R;Sasso, M.P.; Carsana, A.; Confalone, E.; Cosi, C.; Sorrentino, S.; Viola, M.; Palmieri
Nucleic Acids Res. 19, 6469-6474, 1991
A;Title: Molecular cloning of the gene encoding the bovine brain ribonuclease and its ex
A;Reference number: S20066; MUID:92093604; PMID:1754384
A;Accession: S20066
A;Molecule type: DNA
A;Residues: 1-167 <SAS>
A;Cross-references: EMBL:X59767; NID:g150; PIDN:CAA42439.1; PID:g151
R;Watanabe, H.; Katoh, H.; Ishii, M.; Komoda, Y.; Sanda, A.; Takizawa, Y.; Ohgi, K.; Iri
J. Biochem. 104, 939-945, 1988
A;Title: Primary structure of a ribonuclease from bovine brain.
A;Reference number: JX0056; MUID:89214015; PMID:3243767
A;Accession: JX0056
A;Molecule type: protein
A;Residues: 27-154,'S',156-166 <WAT>
A;Experimental source: brain
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase
F;38,67,145/Active site: His, Lys, His #status predicted
F;52-110,66-121,84-136,91-98/Disulfide bonds: #status predicted
F;88/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;155/Binding site: carbohydrate (Thr) (covalent) #status experimental
F;159/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match 21.6%; Score 129.5; DB 2; Length 167;
Best Local Similarity 30.6%; Pred. No. 1e-05;
Matches 37; Conservative 18; Mismatches 43; Indels 23; Gaps 7;

```
Qy          4 ATFQQKHI------INTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINL 57
              | |:::|:       : |  || ::     :  |:|| ||||:  |   |||:|:
Db         32 AKFRRQHMDSGSSSSSNPNYCNQMMKRR-RMTHGRCKPVNTFVHESLDDVKAVCS---QK 87

Qy         58 NVL----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHFA 104
              |:           | :   :  |  |  :  | | | :  :  || | || | | ||||
Db         88 NITCKNGHPNCYQSKSTMSITDCRETGSSKYPNCAYKTSQKQKYITVACEGNPYVPVHFD 147

Qy        105 G 105
              |
Db        148 G 148
```

RESULT 9
S41111
pancreatic ribonuclease - common iguana
C;Species: Iguana iguana (common iguana)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Aug-1998
C;Accession: S41111
R;Zhao, W.; Beintema, J.J.; Hofsteenge, J.
Eur. J. Biochem. 219, 641-646, 1994
A;Title: The amino acid sequence of iguana (Iguana iguana) pancreatic ribonuclease.
A;Reference number: S41111; MUID:94139745; PMID:8307028
A;Accession: S41111
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-119 <ZHA>
C;Superfamily: pancreatic ribonuclease

Query Match 21.2%; Score 127.5; DB 2; Length 119;
Best Local Similarity 29.6%; Pred. No. 1.2e-05;
Matches 34; Conservative 17; Mismatches 51; Indels 13; Gaps 4;

```
Qy          1 QNWATFQQKHI-------INTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAIC-- 51
              |:|::|| |||         |    |: ::     :  :||  |||: :| : :: :|
Db          1 QDWSSFQNKHIDYPETSASNPNAYCDLMMQRR-NLNPTKCKTRNTFVHASPSEIQQVCGS 59

Qy         52 --TGVINLNVLSTTRFQLNTCTRTSIT-PRPCPYSSRTETNYICVKCENQYPVHF 103
                |   :   |  | | |     | |  | |:    |  | : |||  ||||
Db         60 GGTHYEDNLYDSNESFDLTDCKNVGGTAPSSCKYNGTPGTKRIRIACENNQPVHF 114
```

RESULT 10
NRKGR
pancreatic ribonuclease (EC 3.1.27.5) - red kangaroo
N;Alternate names: RNase 1; RNase A
C;Species: Macropus rufus, Megaleia rufa (red kangaroo)
C;Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 04-Oct-1996
C;Accession: A00833
R;Gaastra, W.; Welling, G.W.; Beintema, J.J.
Eur. J. Biochem. 86, 209-217, 1978
A;Title: The amino-acid sequence of kangaroo pancreatic ribonuclease.
A;Reference number: A00833; MUID:78190621; PMID:658039
A;Accession: A00833
A;Molecule type: protein
A;Residues: 1-122 <GAA>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;11,40,117/Active site: His, Lys, His #status predicted
F;25-83,39-94,57-109,64-71/Disulfide bonds: #status predicted
F;61/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 19.8%; Score 119; DB 1; Length 122;
Best Local Similarity 29.8%; Pred. No. 8.2e-05;
Matches 34; Conservative 17; Mismatches 45; Indels 18; Gaps 6;

```
Qy          6 FQQKHI------INTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAIC-------- 51
              ||::|:       ::   || ::     :  |:|| :||||    : | |:|
```

```
Qy          1 QNWATFQQKHIINTP-IICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGV-INLN 58
              |||| ||:||| ||  | |||:| :|||||||||  ||||||||||||||:|   | |
Db          1 QNWAKFQEKHIPNTSNINCNTIMDKSIYIVGGQCKERNTFIISSATTVKAICSGASTNRN 60

Qy         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              |||||||||||| |::  |||||:|||||| |||||||: ||||||||||
Db         61 VLSTTRFQLNTCIRSATAPRPCPYNSRTETNVICVKCENRLPVHFAGIGRC 111


RESULT 3
JX0085
pancreatic ribonuclease (EC 3.1.27.5) - bullfrog
C;Species: Rana catesbeiana (bullfrog)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994
C;Accession: JX0085
R;Nitta, R.; Katayama, N.; Okabe, Y.; Iwama, M.; Watanabe, H.; Abe, Y.; Okazaki, T.; Ohg
J. Biochem. 106, 729-735, 1989
A;Title: Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver.
A;Reference number: JX0085; MUID:90130374; PMID:2613682
A;Accession: JX0085
A;Molecule type: protein
A;Residues: 1-111 <NIT>
C;Superfamily: pancreatic ribonuclease
C;Keywords: hydrolase; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10,35,104/Active site: His, Lys, His #status predicted
F;19-72,34-82,52-97,94-111/Disulfide bonds: #status predicted

  Query Match             61.7%;  Score 370;  DB 2;  Length 111;
  Best Local Similarity   64.9%;  Pred. No. 1.1e-29;
  Matches   72;  Conservative   10;  Mismatches   27;  Indels    2;  Gaps    2;

Qy          1 QNWATFQQKHIINTPII-CNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58
              |||| |::||| :|  | ||||:|  |||||||:||  |||||||   |||||:||  :
Db          1 QNWAKFKEKHIRSTSSIDCNTIMDKAIYIVGGKCKERNTFIISSEDNVKAICSGVSPDRK 60

Qy         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              |||| |:|||| | |||||||||    : | |||||| | |||| |||:|
Db         61 ELSTTSFKLNTCIRDSITPRPCPYHPSPDNNKICVKCEKQLPVHFVGIGKC 111


RESULT 4
A39035
ribonuclease-related anti-tumor protein - northern leopard frog (fragment)
C;Species: Rana pipiens (northern leopard frog)
C;Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993
C;Accession: A39035
R;Ardelt, W.; Mikulski, S.M.; Shogen, K.
J. Biol. Chem. 266, 245-251, 1991
A;Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and earl
A;Reference number: A39035; MUID:91093131; PMID:1985896
A;Accession: A39035
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-104 <ARD>
C;Superfamily: pancreatic ribonuclease

  Query Match             45.1%;  Score 270.5;  DB 2;  Length 104;
  Best Local Similarity   47.7%;  Pred. No. 7.1e-20;
  Matches   53;  Conservative   17;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          1 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58
              ::| |||:||| ||  : |: |:  |::     ||  |||| |     |||| |:| : |
Db          1 EDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56

Qy         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104


RESULT 5
A35932
angiogenin precursor - mouse
N;Alternate names: angiogenesis factor
N;Contains: ribonuclease (EC 3.1.27.-)
C;Species: Mus musculus (house mouse)
C;Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 18-Jun-1999
C;Accession: A35932
R;Bond, M.D.; Vallee, B.L.
Biochem. Biophys. Res. Commun. 171, 988-995, 1990
A;Title: Isolation and sequencing of mouse angiogenin DNA.
A;Reference number: A35932; MUID:91025023; PMID:2222458
A;Accession: A35932
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-145 <BON>
A;Cross-references: GB:U22516; NID:g726325; PIDN:AAA91366.1; PID:g726326
C;Genetics:
A;Introns: #status absent
C;Function:
A;Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues
C;Superfamily: pancreatic ribonuclease
C;Keywords: angiogenesis; hydrolase; nucleic acid degradation; pyroglutamic acid
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-145/Product: angiogenin #status predicted <MAT>
F;25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;37,64,137/Active site: His, Lys, His #status predicted
F;50-104,63-115,81-130/Disulfide bonds: #status predicted

  Query Match             22.8%;  Score 136.5;  DB 1;  Length 145;
  Best Local Similarity   40.3%;  Pred. No. 1.8e-06;
  Matches   31;  Conservative   11;  Mismatches   28;  Indels    7;  Gaps    3;

Qy         33 CKRVNTFIISSATTVKAICTG-----VINLNVLSTTRFQLNTCTRTSITPR-PCPYSSRT 86
              || |||||  : : :||||          ||  :| : ||: ||  |  :|| || | :
Db         63 CKDVNTFIHGNKSNIKAICGANGSPYRENLR-MSKSPFQVTTCKHTGGSPRPPCQYRASA 121

Qy         87 ETNYICVKCENQYPVHF 103
                 :: : |||  ||||
Db        122 GFRHVVIACENGLPVHF 138


RESULT 6
NRWHK
pancreatic ribonuclease (EC 3.1.27.5) - minke whale
N;Alternate names: RNase 1; RNase A
C;Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
C;Accession: A00818
R;Emmens, M.; Welling, G.W.; Beintema, J.J.
Biochem. J. 157, 317-323, 1976
A;Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclease.
A;Reference number: A00818; MUID:76277855; PMID:962870
A;Accession: A00818
A;Molecule type: protein
A;Residues: 1-124 <EMM>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F;76/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

  Query Match             21.9%;  Score 131.5;  DB 1;  Length 124;
  Best Local Similarity   32.5%;  Pred. No. 4.8e-06;
  Matches   38;  Conservative   17;  Mismatches   39;  Indels   23;  Gaps    7;

Qy          6 FQQKHII------NTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 59
              ||::|:        | |  || ::     :  |:|| ||||:  |   |||:|:     ||
Db          8 FQRQHMDSGNSPGNNPNYCNQMMMRR-KMTQGRCKPVNTFVHESLEDVKAVCS---QKNV 63

Qy         60 L----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 103
              |          | :  :  | :|  :  | | | : :  :  :| | || | | ||||
Db         64 LCKNGRTNCYESNSTMHITDCRQTGSSKYPNCAYKTSQKEKHIIVACEGNPYVPVHF 120


RESULT 7
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 7, 2004, 21:38:36 ; Search time 9.98129 Seconds
(without alignments)
1060.090 Million cell updates/sec

Title: US-09-961-400-19
Perfect score: 600
Sequence: 1 QNWATFQQKHIINTPIICNT.....ICVKCENQYPVHFAGIGRCP 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	582.5	97.1	111	2	A27121	ribonuclease-relat
2	451	75.2	111	1	JX0120	ribonuclease-relat
3	370	61.7	111	2	JX0085	pancreatic ribonuc
4	270.5	45.1	104	2	A39035	ribonuclease-relat
5	136.5	22.8	145	1	A35932	angiogenin precurs
6	131.5	21.9	124	1	NRWHK	pancreatic ribonuc
7	129.5	21.6	124	1	NRPG	pancreatic ribonuc
8	129.5	21.6	167	2	S20066	pancreatic-type ri
9	127.5	21.2	119	2	S41111	pancreatic ribonuc
10	119	19.8	122	1	NRKGR	pancreatic ribonuc
11	118.5	19.8	123	1	A43825	angiogenin - pig
12	118.5	19.8	124	1	NRPRH	pancreatic ribonuc
13	116.5	19.4	128	1	NRCU	pancreatic ribonuc
14	116.5	19.4	149	1	NRMS	pancreatic ribonuc
15	114.5	19.1	128	1	NRGPB	pancreatic ribonuc
16	114	19.0	125	1	A32474	angiogenin [valida
17	113.5	18.9	124	1	NRCM	pancreatic ribonuc
18	113.5	18.9	124	1	NRCMM	pancreatic ribonuc
19	113.5	18.9	124	1	NRCMB	pancreatic ribonuc
20	113.5	18.9	128	1	NRHO	pancreatic ribonuc
21	113	18.8	147	1	NRHUAG	angiogenin precurs
22	112.5	18.8	128	1	NRKS	pancreatic ribonuc
23	110.5	18.4	124	2	S08549	ribonuclease - dom
24	109.5	18.2	124	1	NRDEN	pancreatic ribonuc
25	109	18.2	125	1	B43825	angiogenin - rabbi
26	108.5	18.1	124	1	NRGF	pancreatic ribonuc
27	108.5	18.1	124	1	NRDEO	pancreatic ribonuc
28	108.5	18.1	130	2	S22808	pancreatic ribonuc
29	107.5	17.9	124	1	NRWB	pancreatic ribonuc
30	107.5	17.9	158	2	I61900	eosinophil-derived
31	106.5	17.8	124	1	NRBOB	pancreatic ribonuc
32	106.5	17.8	124	1	NREKN	pancreatic ribonuc
33	106.5	17.8	124	2	S07141	pancreatic ribonuc
34	106.5	17.8	150	1	NRBO	pancreatic ribonuc
35	105.5	17.6	119	2	JX0115	pancreatic ribonuc
36	105.5	17.6	124	1	NRSH	pancreatic ribonuc
37	105.5	17.6	152	1	NRRT	pancreatic ribonuc
38	104.5	17.4	124	1	NRCB	pancreatic ribonuc
39	103.5	17.2	125	4	A47498	seminal ribonuclea
40	103.5	17.2	150	1	NRBOS	seminal ribonuclea
41	102.5	17.1	124	1	NRHP	pancreatic ribonuc
42	101	16.8	125	2	S04503	pancreatic ribonuc
43	100.5	16.8	124	1	NRGN	pancreatic ribonuc
44	100.5	16.8	124	1	NRDEF	pancreatic ribonuc
45	100.5	16.8	124	2	S08546	pancreatic ribonuc

ALIGNMENTS

RESULT 1
A27121
ribonuclease-related sialic acid-binding lectin - bullfrog
C;Species: Rana catesbeiana (bullfrog)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 30-Jun-1993
C;Accession: A27121
R;Titani, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kawauchi, H.; Takayanag
Biochemistry 26, 2189-2194, 1987
A;Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana)
A;Reference number: A27121; MUID:87299649; PMID:3304421
A;Accession: A27121
A;Molecule type: protein
A;Residues: 1-111 <TIT>
C;Superfamily: pancreatic ribonuclease
C;Keywords: lectin

Query Match 97.1%; Score 582.5; DB 2; Length 111;
Best Local Similarity 96.4%; Pred. No. 1e-50;
Matches 107; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

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Qy          1 QNWATFQQKHIINTPII-CNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 59
              :|||||||||||||||| ||||:|||||||||||||||||||||||||||||:||
Db          1 ENWATFQQKHIINTPIINCNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60

Qy         60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
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RESULT 2
JX0120
ribonuclease-related sialic acid-binding lectin - Japanese frog
C;Species: Rana japonica (Japanese frog)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JX0120
R;Kamiya, Y.; Oyama, F.; Oyama, R.; Sakakibara, F.; Nitta, K.; Kawauchi, H.; Takayanagi,
J. Biochem. 108, 139-143, 1990
A;Title: Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs.
A;Reference number: JX0120; MUID:91035319; PMID:2229005
A;Accession: JX0120
A;Molecule type: protein
A;Residues: 1-111 <KAM>
A;Experimental source: egg
C;Superfamily: pancreatic ribonuclease
C;Keywords: lectin; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;19-72,34-82,52-97,94-111/Disulfide bonds: #status experimental

Query Match 75.2%; Score 451; DB 1; Length 111;
Best Local Similarity 77.5%; Pred. No. 1e-37;
Matches 86; Conservative 8; Mismatches 15; Indels 2; Gaps 2;

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;       ORGANISM:  Rana pipiens
;       DEVELOPMENTAL STAGE:  Oocyte
US-08-467-955-1

  Query Match             45.1%;  Score 270.5;  DB 1;  Length 104;
  Best Local Similarity   47.7%;  Pred. No. 6.5e-24;
  Matches   53;  Conservative   17;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          1 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58
              ::| |||:||| ||  : |: |:  |::     ||  |||| |    ||||| |:| : |
Db          1 EDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56

Qy         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104


RESULT 15
US-08-891-848-13
; Sequence 13, Application US/08891848
; Patent No. 5955073
;  GENERAL INFORMATION:
;    APPLICANT:  Rybak, Susanna M.
;    APPLICANT:  Youle, Richard J.
;    APPLICANT:  Newton, Dianne L.
;    APPLICANT:  Nicholls, Peter J.
;    TITLE OF INVENTION:  Selective RNase Cytotoxic Reagents
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/891,848
;      FILING DATE:  No. 5955073 yet assigned
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/125,462
;      FILING DATE:  22-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/014,082
;      FILING DATE:  04-FEB-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/779,195
;      FILING DATE:  22-OCT-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/510,696
;      FILING DATE:  20-APR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Weber, Ellen Lauver
;      REGISTRATION NUMBER:  32,762
;      REFERENCE/DOCKET NUMBER:  015280-110310US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  104 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  Protein
;      LOCATION:  1..104
;      OTHER INFORMATION:  /label= Onc
;      OTHER INFORMATION:  /note= "Onconase from Rana pipiens"
US-08-891-848-13

  Query Match             45.1%;  Score 270.5;  DB 2;  Length 104;
  Best Local Similarity   47.7%;  Pred. No. 6.5e-24;
  Matches   53;  Conservative   17;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          1 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58
              ::| |||:||| ||  : |: |:  |::     ||  |||| |    ||||| |:| : |
Db          1 EDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56

Qy         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104


Search completed:  May  7, 2004, 21:40:46
Job time :  13.7596 secs
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Rana pipiens
; DEVELOPMENTAL STAGE: Embryo
US-08-283-971-1

Query Match 45.1%; Score 270.5; DB 1; Length 104;
Best Local Similarity 47.7%; Pred. No. 6.5e-24;
Matches 53; Conservative 17; Mismatches 32; Indels 9; Gaps 4;

Qy 1 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58
::| |||:||| || : |: |: |:: || |||| | |||| |:| : |
Db 1 EDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56

Qy 59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
||:|: | |: | ::| ||| | : || || |||| |||| |:| |
Db 57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104

RESULT 13
US-07-921-619-1
; Sequence 1, Application US/07921619
; Patent No. 5595734
; GENERAL INFORMATION:
; APPLICANT: Ardelt Ph.D, Wojciech J.
; APPLICANT: Mikulski, Stanislaw M.
; TITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark H. Jay, P.C.
; STREET: P.O. Box 020083, General Post Office
; CITY: Brooklyn
; STATE: New York
; COUNTRY: USA
; ZIP: 11202-0002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/921,619
; FILING DATE: 19920728
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/178,118
; FILING DATE: 06-APR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/436,141
; FILING DATE: 13-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Jay, Mark H.
; REGISTRATION NUMBER: 27507
; REFERENCE/DOCKET NUMBER: 5005 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 718-625-0399
; TELEFAX: 718-625-0399
; TELEX: No. 5595734 Applicable
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Rana pipiens
; DEVELOPMENTAL STAGE: Embryo
US-07-921-619-1

Query Match 45.1%; Score 270.5; DB 1; Length 104;
Best Local Similarity 47.7%; Pred. No. 6.5e-24;
Matches 53; Conservative 17; Mismatches 32; Indels 9; Gaps 4;

Qy 1 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58
::| |||:||| || : |: |: |:: || |||| | |||| |:| : |
Db 1 EDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56

Qy 59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
||:|: | |: | ::| ||| | : || || |||| |||| |:| |
Db 57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104

RESULT 14
US-08-467-955-1
; Sequence 1, Application US/08467955
; Patent No. 5728805
; GENERAL INFORMATION:
; APPLICANT: Ardelt Ph.D, Wojciech J.
; TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark H. Jay, P.A.
; STREET: P.O. Box E
; CITY: Short Hills
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07078-0383
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,955
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/178,118
; FILING DATE: 06-APR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/436,141
; FILING DATE: 13-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/814,332
; FILING DATE: 03-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/283,970
; FILING DATE: 01-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jay, Mark H.
; REGISTRATION NUMBER: 27507
; REFERENCE/DOCKET NUMBER: 5007 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-912-9066
; TELEFAX: 201-912-0442
; TELEX: No. 5728805 Applicable
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:

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;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/875,811
;       FILING DATE:  19-FEB-1998
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  WO PCT/US97/02588
;       FILING DATE:  19-FEB-1997
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 60/011,800
;       FILING DATE:  21-FEB-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Faris, Susan K.
;       REGISTRATION NUMBER:  41,739
;       REFERENCE/DOCKET NUMBER:  015280-244100US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 576-0200
;       TELEFAX:  (415) 576-0300
;   INFORMATION FOR SEQ ID NO:  63:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  129 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-875-811-63

  Query Match             45.6%;  Score 273.5;  DB 3;  Length 129;
  Best Local Similarity   48.6%;  Pred. No. 3.8e-24;
  Matches   54;  Conservative   16;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          1 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58
              |:| |||:||| ||  : |: |:  |::     ||  |||| |    |||| |:| : |
Db         26 QDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 81

Qy         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         82 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 129


RESULT 11
US-08-875-811-43
; Sequence 43, Application US/08875811
; Patent No. 6045793
;  GENERAL INFORMATION:
;    APPLICANT:  Rybak, Susanna M.
;    APPLICANT:  Newton, Dianne L.
;    APPLICANT:  Boque, Lluis
;    APPLICANT:  Wlodawer, Alexander
;    TITLE OF INVENTION:  Recombinant Ribonuclease Proteins
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/875,811
;      FILING DATE:  19-FEB-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/02588
;      FILING DATE:  19-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/011,800
;      FILING DATE:  21-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Faris, Susan K.
;      REGISTRATION NUMBER:  41,739
;      REFERENCE/DOCKET NUMBER:  015280-244100US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  43:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  379 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-875-811-43

  Query Match             45.6%;  Score 273.5;  DB 3;  Length 379;
  Best Local Similarity   48.6%;  Pred. No. 1.4e-23;
  Matches   54;  Conservative   16;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          1 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58
              |:| |||:||| ||  : |: |:  |::     ||  |||| |    |||| |:| : |
Db         26 QDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 81

Qy         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         82 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 129


RESULT 12
US-08-283-971-1
; Sequence 1, Application US/08283971
; Patent No. 5529775
;  GENERAL INFORMATION:
;    APPLICANT:  Ardelt Ph.D, Wojciech J.
;    APPLICANT:  Mikulski, Stanislaw M.
;    TITLE OF INVENTION:  PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mark H. Jay, P.C.
;      STREET:  P.O. Box 020083, General Post Office
;      CITY:  Brooklyn
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  11202-0002
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/283,971
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/921,180
;      FILING DATE:  30-JUL-1992
;      APPLICATION NUMBER:  US 07/178,118
;      FILING DATE:  06-APR-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/436,141
;      FILING DATE:  13-NOV-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jay, Mark H.
;      REGISTRATION NUMBER:  27507
;      REFERENCE/DOCKET NUMBER:  5006 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  718-625-0399
;      TELEFAX:  718-625-0399
;      TELEX:  No. 5529775 Applicable
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  104 amino acids
;      TYPE:  amino acid
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Qy          59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
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Db          57 VLTTSEFYLSDC---NVTCRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104


RESULT 8
US-08-626-288-1
; Sequence 1, Application US/08626288
; Patent No. 6649392
;  GENERAL INFORMATION:
;    APPLICANT:  Youle, Richard
;    APPLICANT:  Vasandani, Veena
;    APPLICANT:  Wu, Yon-Neng
;    APPLICANT:  Boix, Ester
;    APPLICANT:  Ardelt, Wojeiech
;    TITLE OF INVENTION:  A Mutant Form of Cytotoxic Protein Which
;    TITLE OF INVENTION:  Allows Production by Recombinant Methods
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew
;      STREET:  One Market Plaza, Steuart Street Tower
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105-1492
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/626,288
;      FILING DATE:  No. 6649392 yet assigned
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ran, David B.
;      REGISTRATION NUMBER:  38,589
;      REFERENCE/DOCKET NUMBER:  15280-267
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 543-9600
;      TELEFAX:  (415) 543-5043
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  104 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-626-288-1

  Query Match             45.6%;  Score 273.5;  DB 4;  Length 104;
  Best Local Similarity   48.6%;  Pred. No. 2.9e-24;
  Matches   54;  Conservative   16;  Mismatches   32;  Indels    9;  Gaps    4;

Qy           1 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58
               |:| |||:||| ||  : |: |:  |::     ||  |||| |    |||| |:| : |
Db           1 QDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56

Qy          59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
               ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db          57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104


RESULT 9
US-09-095-429-1
; Sequence 1, Application US/09095429
; Patent No. 6649393
;  GENERAL INFORMATION:
;    APPLICANT:  Youle, Richard
;    APPLICANT:  Vasandani, Veena
;    APPLICANT:  Wu, Yon-Neng
;    APPLICANT:  Boix, Ester
;    APPLICANT:  Ardelt, Wojeiech
;    TITLE OF INVENTION:  A Mutant Form of Cytotoxic Protein Which
;    TITLE OF INVENTION:  Allows Production by Recombinant Methods
;    NUMBER OF SEQUENCES:  3
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew
;      STREET:  One Market Plaza, Steuart Street Tower
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105-1492
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/095,429
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/626,288
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ran, David B.
;      REGISTRATION NUMBER:  38,589
;      REFERENCE/DOCKET NUMBER:  15280-267
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 543-9600
;      TELEFAX:  (415) 543-5043
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  104 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-095-429-1

  Query Match             45.6%;  Score 273.5;  DB 4;  Length 104;
  Best Local Similarity   48.6%;  Pred. No. 2.9e-24;
  Matches   54;  Conservative   16;  Mismatches   32;  Indels    9;  Gaps    4;

Qy           1 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58
               |:| |||:||| ||  : |: |:  |::     ||  |||| |    |||| |:| : |
Db           1 QDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56

Qy          59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
               ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
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RESULT 10
US-08-875-811-63
; Sequence 63, Application US/08875811
; Patent No. 6045793
;  GENERAL INFORMATION:
;    APPLICANT:  Rybak, Susanna M.
;    APPLICANT:  Newton, Dianne L.
;    APPLICANT:  Boque, Lluis
;    APPLICANT:  Wlodawer, Alexander
;    TITLE OF INVENTION:  Recombinant Ribonuclease Proteins
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
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; DEVELOPMENTAL STAGE: Oocyte
US-08-467-955-2

Query Match 46.8%; Score 280.5; DB 1; Length 104;
Best Local Similarity 48.6%; Pred. No. 4.5e-25;
Matches 54; Conservative 17; Mismatches 31; Indels 9; Gaps 4;

Qy 1 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58
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Db 1 EDWLTFQKKHVTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56

Qy 59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
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Db 57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGRC 104

RESULT 4
US-09-394-268-1
; Sequence 1, Application US/09394268
; Patent No. 6175003
; GENERAL INFORMATION:
; APPLICANT: Saxena, Shailendra K
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING RIBONUCLEASES AND METHODS OF
; TITLE OF INVENTION: MAKING THEM
; FILE REFERENCE: 5013
; CURRENT APPLICATION NUMBER: US/09/394,268
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Rana pipiens
US-09-394-268-1

Query Match 45.6%; Score 273.5; DB 3; Length 104;
Best Local Similarity 48.6%; Pred. No. 2.9e-24;
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

Qy 1 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58
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Db 1 QDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56

Qy 59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
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Db 57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104

RESULT 5
US-09-394-268-2
; Sequence 2, Application US/09394268
; Patent No. 6175003
; GENERAL INFORMATION:
; APPLICANT: Saxena, Shailendra K
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING RIBONUCLEASES AND METHODS OF
; TITLE OF INVENTION: MAKING THEM
; FILE REFERENCE: 5013
; CURRENT APPLICATION NUMBER: US/09/394,268
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SEQ ID NO:1 with Leu at position 23 and Cys at
; OTHER INFORMATION: position 72
US-09-394-268-2

Query Match 45.6%; Score 273.5; DB 3; Length 104;
Best Local Similarity 49.5%; Pred. No. 2.9e-24;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

Qy 1 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58
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Db 1 QDWLTFQKKHITNTRDVDCDNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56

Qy 59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
||:|: | |: | ::| ||| | : || || |||| |||| |:| |
Db 57 VLTTSEFYLSDC---NVTCRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104

RESULT 6
US-09-687-748-1
; Sequence 1, Application US/09687748
; Patent No. 6423515
; GENERAL INFORMATION:
; APPLICANT: Saxena, Shailendra K
; TITLE OF INVENTION: METHODS OF MAKING NUCLEIC ACIDS ENCODING RIBONUCLEASES
; FILE REFERENCE: 5013 US 01
; CURRENT APPLICATION NUMBER: US/09/687,748
; CURRENT FILING DATE: 2000-10-14
; PRIOR APPLICATION NUMBER: 09/394,268
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Rana pipiens
US-09-687-748-1

Query Match 45.6%; Score 273.5; DB 4; Length 104;
Best Local Similarity 48.6%; Pred. No. 2.9e-24;
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

Qy 1 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58
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Qy 59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
||:|: | |: | ::| ||| | : || || |||| |||| |:| |
Db 57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104

RESULT 7
US-09-687-748-2
; Sequence 2, Application US/09687748
; Patent No. 6423515
; GENERAL INFORMATION:
; APPLICANT: Saxena, Shailendra K
; TITLE OF INVENTION: METHODS OF MAKING NUCLEIC ACIDS ENCODING RIBONUCLEASES
; FILE REFERENCE: 5013 US 01
; CURRENT APPLICATION NUMBER: US/09/687,748
; CURRENT FILING DATE: 2000-10-14
; PRIOR APPLICATION NUMBER: 09/394,268
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SEQ ID NO:1 with Leu at position 23 and Cys at
; OTHER INFORMATION: position 72
US-09-687-748-2

Query Match 45.6%; Score 273.5; DB 4; Length 104;
Best Local Similarity 49.5%; Pred. No. 2.9e-24;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

Qy 1 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58
|:| |||:||| || : |: |: |:: || |||| | ||||| |:| : |
Db 1 QDWLTFQKKHITNTRDVDCDNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56

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;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  Protein
;      LOCATION:  1..111
;      OTHER INFORMATION:  /note= "Frog Lectin from Rana
;      OTHER INFORMATION:  catesbeiana"
US-08-891-848-12

  Query Match             97.1%;  Score 582.5;  DB 2;  Length 111;
  Best Local Similarity   96.4%;  Pred. No. 6.4e-60;
  Matches  107;  Conservative    3;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 QNWATFQQKHIINTPII-CNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 59
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Qy         60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
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Db         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111


RESULT 2
US-08-875-811-8
; Sequence 8, Application US/08875811
; Patent No. 6045793
;  GENERAL INFORMATION:
;    APPLICANT:  Rybak, Susanna M.
;    APPLICANT:  Newton, Dianne L.
;    APPLICANT:  Boque, Lluis
;    APPLICANT:  Wlodawer, Alexander
;    TITLE OF INVENTION:  Recombinant Ribonuclease Proteins
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/875,811
;      FILING DATE:  19-FEB-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/02588
;      FILING DATE:  19-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/011,800
;      FILING DATE:  21-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Faris, Susan K.
;      REGISTRATION NUMBER:  41,739
;      REFERENCE/DOCKET NUMBER:  015280-244100US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  111 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  Protein
;      LOCATION:  1..111
;      OTHER INFORMATION:  /note= "Frog Lectin from Rana
;      OTHER INFORMATION:  catesbeiana"
US-08-875-811-8

  Query Match             97.1%;  Score 582.5;  DB 3;  Length 111;
  Best Local Similarity   96.4%;  Pred. No. 6.4e-60;
  Matches  107;  Conservative    3;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 QNWATFQQKHIINTPII-CNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 59
              :|||||||||||||||| |||:|||||||||||||||||||||||||||||||:||
Db          1 ENWATFQQKHIINTPIINCNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60

Qy         60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111


RESULT 3
US-08-467-955-2
; Sequence 2, Application US/08467955
; Patent No. 5728805
;  GENERAL INFORMATION:
;    APPLICANT:  Ardelt Ph.D, Wojciech J.
;    TITLE OF INVENTION:  PHARMACEUTICALS AND METHOD FOR MAKING THEM
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Mark H. Jay, P.A.
;      STREET:  P.O. Box E
;      CITY:  Short Hills
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07078-0383
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/467,955
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/178,118
;      FILING DATE:  06-APR-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/436,141
;      FILING DATE:  13-NOV-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/814,332
;      FILING DATE:  03-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/283,970
;      FILING DATE:  01-AUG-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jay, Mark H.
;      REGISTRATION NUMBER:  27507
;      REFERENCE/DOCKET NUMBER:  5007 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-912-9066
;      TELEFAX:  201-912-0442
;      TELEX:  No. 5728805 Applicable
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  104 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  N
;    ANTI-SENSE:  N
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  Rana pipiens
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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:28:45 ; Search time 12.7596 Seconds
(without alignments)
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Title: US-09-961-400-19
Perfect score: 600
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Scoring table: BLOSUM62
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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	582.5	97.1	111	2	US-08-891-848-12	Sequence 12, Appl
2	582.5	97.1	111	3	US-08-875-811-8	Sequence 8, Appli
3	280.5	46.8	104	1	US-08-467-955-2	Sequence 2, Appli
4	273.5	45.6	104	3	US-09-394-268-1	Sequence 1, Appli
5	273.5	45.6	104	3	US-09-394-268-2	Sequence 2, Appli
6	273.5	45.6	104	4	US-09-687-748-1	Sequence 1, Appli
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8	273.5	45.6	104	4	US-08-626-288-1	Sequence 1, Appli
9	273.5	45.6	104	4	US-09-095-429-1	Sequence 1, Appli
10	273.5	45.6	129	3	US-08-875-811-63	Sequence 63, Appl
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13	270.5	45.1	104	1	US-07-921-619-1	Sequence 1, Appli
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18	270.5	45.1	105	3	US-08-875-811-39	Sequence 39, Appl
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27	268.5	44.8	251	3	US-08-875-811-59	Sequence 59, Appl
28	268.5	44.8	254	3	US-08-875-811-61	Sequence 61, Appl
29	268.5	44.8	355	3	US-08-875-811-49	Sequence 49, Appl
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31	268.5	44.8	355	3	US-08-875-811-64	Sequence 64, Appl
32	268.5	44.8	366	3	US-08-875-811-55	Sequence 55, Appl
33	263.5	43.9	105	3	US-08-875-811-24	Sequence 24, Appl
34	263.5	43.9	105	3	US-08-875-811-26	Sequence 26, Appl
35	259.5	43.2	358	3	US-08-875-811-45	Sequence 45, Appl
36	259.5	43.2	365	3	US-08-875-811-53	Sequence 53, Appl
37	245.5	40.9	107	3	US-08-875-811-20	Sequence 20, Appl
38	235.5	39.2	111	3	US-08-875-811-22	Sequence 22, Appl
39	232	38.7	114	3	US-09-223-118-3	Sequence 3, Appli
40	223.5	37.2	360	3	US-08-875-811-47	Sequence 47, Appl
41	223	37.2	114	3	US-09-223-118-2	Sequence 2, Appli
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43	221	36.8	114	3	US-09-223-118-4	Sequence 4, Appli
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45	202	33.7	83	4	US-09-071-672-3	Sequence 3, Appli

ALIGNMENTS

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RESULT 1
US-08-891-848-12
; Sequence 12, Application US/08891848
; Patent No. 5955073
;  GENERAL INFORMATION:
;    APPLICANT:  Rybak, Susanna M.
;    APPLICANT:  Youle, Richard J.
;    APPLICANT:  Newton, Dianne L.
;    APPLICANT:  Nicholls, Peter J.
;    TITLE OF INVENTION:  Selective RNase Cytotoxic Reagents
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/891,848
;      FILING DATE:  No. 5955073 yet assigned
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/125,462
;      FILING DATE:  22-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/014,082
;      FILING DATE:  04-FEB-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/779,195
;      FILING DATE:  22-OCT-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/510,696
;      FILING DATE:  20-APR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Weber, Ellen Lauver
;      REGISTRATION NUMBER:  32,762
;      REFERENCE/DOCKET NUMBER:  015280-110310US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  111 amino acids
;      TYPE:  amino acid
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OS Rana pipiens.
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PN WO9738112-A1.
XX
PD 16-OCT-1997.
XX
PF 04-APR-1997; 97WO-US005675.
XX
PR 04-APR-1996; 96US-00626288.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Youle RJ, Vasandani VM, Wu Y, Boix E, Ardelt W;
XX
DR WPI; 1997-512725/47.
XX
PT Recombinant Onc protein with glutamine residue at position 1 - useful as
PT antitumour and antiviral agent, also as cell culture selection agent.
XX
PS Claim 1; Page 28; 35pp; English.
XX
CC This sequence represents a recombinant Onc protein comprising a 104 amino
CC acid sequence having Gln at position 1. Onc, a ribonuclease from Rana
CC pipiens oocytes, is known as an antitumour agent (e.g. for treating
CC pancreatic cancer) and inhibitor of human immunodeficiency virus type-1
CC replication. It can be used therapeutically or as a cell-culture
CC selection agent, e.g. to identify gene therapy compositions able to
CC inhibit tumour growth
XX
SQ Sequence 104 AA;

Query Match 45.6%; Score 273.5; DB 2; Length 104;
Best Local Similarity 48.6%; Pred. No. 5.5e-23;
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

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Qy          1 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58
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Db          1 QDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56

Qy         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
```

RESULT 15
AAB31667
ID AAB31667 standard; protein; 104 AA.
XX
AC AAB31667;
XX
DT 30-APR-2001 (first entry)
XX
DE Amino acid sequence of a modified frog ribonuclease protein.
XX
KW Frog; ribonuclease; ranpirnase; RNase.
XX
OS Synthetic.
OS Rana pipiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 23
FT /note= "wild type Met changed to Leu"
FT Misc-difference 72
FT /note= "wild type Ser changed to Cys"
XX
PN US6175003-B1.
XX
PD 16-JAN-2001.
XX
PF 10-SEP-1999; 99US-00394268.
XX
PR 10-SEP-1999; 99US-00394268.
XX
PA (ALFA-) ALFACELL CORP.
XX
PI Saxena SK;
XX
DR WPI; 2001-167808/17.
XX
PT New nucleic acids encoding a ribonuclease (Rnase), useful for the precise
PT targeting of Rnase to a predetermined cell receptor.
XX
PS Claim 2; Col 5-6; 7pp; English.
XX
CC The present sequence represents a modifed frog ribonuclease protein
CC (ranpirnase) (RNase). The synthetic ribonuclease comprises a cysteine
CC which facilitates the chemical linking of a targeting molecule by the
CC single reactive sulfhydryl group. The specification describes a method
CC for the production of ranpirnase using DNA technology instead of
CC processing biological material. The re-engineering of the protein
CC molecule allows easier attachment to a targeting molecule thereby making
CC it possible for the ribonuclease to be delivered to a particular cell
CC receptor where it might be most effective
XX
SQ Sequence 104 AA;

Query Match 45.6%; Score 273.5; DB 4; Length 104;
Best Local Similarity 49.5%; Pred. No. 5.5e-23;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

```
Qy          1 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58
              |:| |||:||| ||  : |: ||  |::     ||  |||| |    ||||| |:| : |
Db          1 QDWLTFQKKHITNTRDVDCDNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56

Qy         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         57 VLTTSEFYLSDC---NVTCRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
```

Search completed: May 7, 2004, 21:38:29
Job time : 47.9224 secs

```
KW   covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
KW   Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
KW   recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
KW   autoimmune disease.
XX
OS   Rana pipiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
FT                   /note= "Met not found in wild type RaPLR1"
XX
PN   WO9950398-A2.
XX
PD   07-OCT-1999.
XX
PF   26-MAR-1999;   99WO-US006641.
XX
PR   27-MAR-1998;   98US-0079751P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL;
XX
DR   WPI; 1999-610847/52.
DR   N-PSDB; AAZ08126.
XX
PT   New recombinant ribonucleases, used for killing target cells, e.g. for
PT   treating cancers, viral infections or autoimmune diseases.
XX
PS   Claim 34; Page 57; 71pp; English.
XX
CC   The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1)
CC   protein with Met at position 1. Carboxy terminal end of recombinant
CC   RaPLR1 has a covalently bound ligand binding moiety, which can be a LL2
CC   antibody directed against CD22 on cancerous B cells or human chorionic
CC   gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant
CC   ribonucleases can be expressed in bacteria without an N-terminal
CC   methionine due to the presence of a signal peptide that is cleaved by
CC   bacteria. The soluble expression of ribonuclease allows the proteins to
CC   be fused in-frame with ligand binding moieties to form cytotoxic fusion
CC   proteins. They can be used for treatment of cancer and autoimmune
CC   diseases
XX
SQ   Sequence 105 AA;

  Query Match             46.2%;  Score 277.5;  DB 2;  Length 105;
  Best Local Similarity   48.6%;  Pred. No. 2e-23;
  Matches   54;  Conservative   16;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          1 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58
              |:| |||:||: ||  : || |:  |::     ||  |||| |    ||||| |:| : |
Db          2 QDWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 57

Qy         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         58 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105


RESULT 13
AAY28879
ID   AAY28879 standard; protein; 127 AA.
XX
AC   AAY28879;
XX
DT   25-JAN-2000  (first entry)
XX
DE   Rana pipiens Clone 5a1b ribonuclease.
XX
KW   Rana pipiens ribonuclease Clone 5a1b; RaPLR1; covalently bound; RNase;
KW   LL2 antibody; ligand binding moiety; CD22; cancerous B cell; onconase;
KW   Kaposi's Sarcoma; human chorionic gonadotrophin; hCG; cancer;
KW   recombinant ribonuclease; frog; signal peptide; cytotoxic fusion protein;
KW   autoimmune disease.
XX
OS   Rana pipiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /label= Signal_peptide
FT                   /note= "Putative"
FT   Protein         24. .127
FT                   /label= Rana_pipiens_Clone_5a1b_ribonuclease
XX
PN   WO9950398-A2.
XX
PD   07-OCT-1999.
XX
PF   26-MAR-1999;   99WO-US006641.
XX
PR   27-MAR-1998;   98US-0079751P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL;
XX
DR   WPI; 1999-610847/52.
DR   N-PSDB; AAZ08136.
XX
PT   New recombinant ribonucleases, used for killing target cells, e.g. for
PT   treating cancers, viral infections or autoimmune diseases.
XX
PS   Disclosure; Page 69; 71pp; English.
XX
CC   The present sequence is a Rana pipiens Clone 5a1b ribonuclease (RaPLR1).
CC   It is encoded by Clone 5a1b cDNA obtained from Rana pipiens liver mRNA
CC   library. It exhibits differences with Onconase (RTM) at amino acid
CC   residues 11, 20, 85 and 103. Carboxy terminal end of RaPLR1 has a
CC   covalently bound ligand binding moiety, which can be a LL2 antibody
CC   directed against CD22 on cancerous B cells or human chorionic
CC   gonadotrophin (hCG) effective against Kaposi's Sarcoma cells. Recombinant
CC   ribonucleases can be expressed in bacteria without an N-terminal
CC   methionine due to the presence of a signal peptide that is cleaved by
CC   bacteria. The soluble expression of ribonuclease allows the proteins to
CC   be fused in-frame with ligand binding moieties to form cytotoxic fusion
CC   proteins. They can be used for treatment of cancer and autoimmune
CC   diseases
XX
SQ   Sequence 127 AA;

  Query Match             46.2%;  Score 277.5;  DB 2;  Length 127;
  Best Local Similarity   48.6%;  Pred. No. 2.5e-23;
  Matches   54;  Conservative   16;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          1 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58
              |:| |||:||: ||  : || |:  |::     ||  |||| |    ||||| |:| : |
Db         24 QDWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 79

Qy         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         80 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 127


RESULT 14
AAW30301
ID   AAW30301 standard; protein; 104 AA.
XX
AC   AAW30301;
XX
DT   09-JUN-1998  (first entry)
XX
DE   Recombinant onc protein.
XX
KW   Onc; oncanase; ribonuclease; frog; antitumour; pancreatic cancer;
KW   human immunodeficiency virus type-1; HIV1; replication.
XX
```

```
ID   AAY28869 standard; protein; 105 AA.
XX
AC   AAY28869;
XX
DT   25-JAN-2000  (first entry)
XX
DE   Recombinant Met(-1) RaPLR1 Met23Leu-(His)6 protein.
XX
KW   Recombinant Met(-1) Rana pipiens ribonuclease Met23Leu-(His)6; RaPLR1;
KW   CD22; covalently bound; LL2 antibody; ligand binding moiety; RNase;
KW   cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG;
KW   signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
KW   cancer; frog; autoimmune disease.
XX
OS   Rana pipiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
FT                   /note= "Met not found in wild type RaPLR1"
FT   Misc-difference 1
FT                   /note= "(His)6 histidine tag attached to N-terminal Met"
FT   Misc-difference 24
FT                   /note= "Wild type Met replaced with Leu"
XX
PN   WO9950398-A2.
XX
PD   07-OCT-1999.
XX
PF   26-MAR-1999;   99WO-US006641.
XX
PR   27-MAR-1998;   98US-0079751P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL;
XX
DR   WPI; 1999-610847/52.
DR   N-PSDB; AAZ08127.
XX
PT   New recombinant ribonucleases, used for killing target cells, e.g. for
PT   treating cancers, viral infections or autoimmune diseases.
XX
PS   Claim 4; Page 59; 71pp; English.
XX
CC   The present sequence is a recombinant Rana pipiens ribonuclease protein
CC   (RaPLR1) with Met at position 1 attached to (His)6 tag and Met24Leu.
CC   Carboxy terminal end of recombinant RaPLR1 has a covalently bound ligand
CC   binding moiety, which can be a LL2 antibody directed against CD22 on
CC   cancerous B cells or human chorionic gonadotrophin (hCG) effective
CC   against Kaposi's sarcoma cells. Recombinant ribonucleases can be
CC   expressed in bacteria without an N-terminal methionine due to the
CC   presence of a signal peptide that is cleaved by bacteria. The soluble
CC   expression of ribonuclease allows the proteins to be fused in-frame with
CC   ligand binding moieties to form cytotoxic fusion proteins. They can be
CC   used for treatment of cancer and autoimmune diseases
XX
SQ   Sequence 105 AA;

  Query Match             46.6%;  Score 279.5;  DB 2;  Length 105;
  Best Local Similarity   49.5%;  Pred. No. 1.2e-23;
  Matches   55;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          1 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58
              |:| |||:||: ||  : || ||  |::     ||  |||| |    ||||| |:| : |
Db          2 QDWLTFQKKHLTNTRDVDCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 57

Qy         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         58 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105


RESULT 11
AAY28865
ID   AAY28865 standard; protein; 104 AA.
XX
AC   AAY28865;
XX
DT   25-JAN-2000  (first entry)
XX
DE   Rana pipiens liver ribonuclease (RaPLR1).
XX
KW   Rana pipiens liver ribonuclease; RaPLR1; covalently bound; LL2 antibody;
KW   ligand binding moiety; CD22; cancerous B cell; Kaposi's Sarcoma; frog;
KW   human chorionic gonadotrophin; hCG; recombinant ribonuclease; RNase;
KW   signal peptide; cytotoxic fusion protein; cancer; autoimmune disease.
XX
OS   Rana pipiens.
XX
PN   WO9950398-A2.
XX
PD   07-OCT-1999.
XX
PF   26-MAR-1999;   99WO-US006641.
XX
PR   27-MAR-1998;   98US-0079751P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL;
XX
DR   WPI; 1999-610847/52.
DR   N-PSDB; AAZ08124.
XX
PT   New recombinant ribonucleases, used for killing target cells, e.g. for
PT   treating cancers, viral infections or autoimmune diseases.
XX
PS   Claim 1; Page 55; 71pp; English.
XX
CC   The present sequence is Rana pipiens liver ribonuclease (RaPLR1) protein.
CC   Carboxy terminal end of RaPLR1 has a covalently bound ligand binding
CC   moiety, which can be a LL2 antibody directed against CD22 on cancerous B
CC   cells or human chorionic gonadotrophin (hCG) effective against Kaposi's
CC   Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria
CC   without an N-terminal methionine due to the presence of a signal peptide
CC   that is cleaved by bacteria. The soluble expression of ribonuclease
CC   allows the proteins to be fused in-frame with ligand binding moieties to
CC   form cytotoxic fusion proteins. They can be used for treatment of cancer
CC   and autoimmune diseases
XX
SQ   Sequence 104 AA;

  Query Match             46.2%;  Score 277.5;  DB 2;  Length 104;
  Best Local Similarity   48.6%;  Pred. No. 1.9e-23;
  Matches   54;  Conservative   16;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          1 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58
              |:| |||:||: ||  : || |:  |::     ||  |||| |    ||||| |:| : |
Db          1 QDWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56

Qy         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104


RESULT 12
AAY28867
ID   AAY28867 standard; protein; 105 AA.
XX
AC   AAY28867;
XX
DT   25-JAN-2000  (first entry)
XX
DE   Recombinant Met(-1) RaPLR1.
XX
KW   Recombinant Met(-1) Rana pipiens ribonuclease; RaPLR1; CD22; RNase;
```

```
CC   (Rana catesbeiana) lectin used to describe the method of the invention
XX
SQ   Sequence 111 AA;

  Query Match             97.1%;  Score 582.5;  DB 2;  Length 111;
  Best Local Similarity   96.4%;  Pred. No. 6.5e-58;
  Matches  107;  Conservative    3;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 QNWATFQQKHIINTPII-CNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 59
              :|||||||||||||||| |||||:|||||||||||||||||||||||||||||||||||:||
Db          1 ENWATFQQKHIINTPIINCNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60

Qy         60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111


RESULT 8
AAW06544
ID   AAW06544 standard; protein; 104 AA.
XX
AC   AAW06544;
XX
DT   22-AUG-1997  (first entry)
XX
DE   Antitumour protein from Rana pipiens oocytes.
XX
KW   Tumour; chemotherapy; radiotherapy; frog.
XX
OS   Rana pipiens.
XX
PN   WO9639428-A1.
XX
PD   12-DEC-1996.
XX
PF   03-JUN-1996;   96WO-US008304.
XX
PR   06-JUN-1995;   95US-00467955.
XX
PA   (ALFA-) ALFACELL CORP.
XX
PI   Ardelt WJ;
XX
DR   WPI; 1997-043063/04.
XX
PT   Antitumour proteins from Rana pipiens oocyte(s) - have fewer
PT   disadvantages than chemotherapy, surgery and radiotherapy.
XX
PS   Claim 8; Page 28; 45pp; English.
XX
CC   The present sequence is a specifically claimed example of an antitumour
CC   protein from the generic protein in AAW18224, with the molecular weight
CC   12000. This is one of two preferred proteins (the other in AAW06543) that
CC   have been isolated from Rana pipiens oocytes. Both proteins have a
CC   blocked amino terminal group and are essentially free of carbohydrates.
CC   The proteins are used to treat tumours. Use of the peptides has fewer
CC   disadvantages than chemotherapy, radiotherapy and surgery in the
CC   treatment of tumours
XX
SQ   Sequence 104 AA;

  Query Match             46.8%;  Score 280.5;  DB 2;  Length 104;
  Best Local Similarity   48.6%;  Pred. No. 8.8e-24;
  Matches   54;  Conservative   17;  Mismatches   31;  Indels    9;  Gaps    4;

Qy          1 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58
              ::| |||:||: ||  : || |:  |::     ||  |||| |    ||||| |:| : |
Db          1 EDWLTFQKKHVTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56

Qy         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:|||
Db         57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGRC 104


RESULT 9
AAY28866
ID   AAY28866 standard; protein; 104 AA.
XX
AC   AAY28866;
XX
DT   25-JAN-2000  (first entry)
XX
DE   Recombinant RaPLR1 Met23Leu amino acid sequence.
XX
KW   Recombinant Rana pipiens ribonuclease; RaPLR1 Met23Leu; covalently bound;
KW   LL2 antibody; ligand binding moiety; CD22; cancerous B cell; RNase;
KW   Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
KW   recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
KW   autoimmune disease.
XX
OS   Rana pipiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 23
FT                   /note= "Wild type Met replaced with Leu"
XX
PN   WO9950398-A2.
XX
PD   07-OCT-1999.
XX
PF   26-MAR-1999;   99WO-US006641.
XX
PR   27-MAR-1998;   98US-0079751P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL;
XX
DR   WPI; 1999-610847/52.
DR   N-PSDB; AAZ08125.
XX
PT   New recombinant ribonucleases, used for killing target cells, e.g. for
PT   treating cancers, viral infections or autoimmune diseases.
XX
PS   Claim 34; Page 56; 71pp; English.
XX
CC   The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1)
CC   protein with Met23Leu. Carboxy terminal end of recombinant RaPLR1 has a
CC   covalently bound ligand binding moiety, which can be a LL2 antibody
CC   directed against CD22 on cancerous B cells or human chorionic
CC   gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant
CC   ribonucleases can be expressed in bacteria without an N-terminal
CC   methionine due to the presence of a signal peptide that is cleaved by
CC   bacteria. The soluble expression of ribonuclease allows the proteins to
CC   be fused in-frame with ligand binding moieties to form cytotoxic fusion
CC   proteins. They can be used for treatment of cancer and autoimmune
CC   diseases
XX
SQ   Sequence 104 AA;

  Query Match             46.6%;  Score 279.5;  DB 2;  Length 104;
  Best Local Similarity   49.5%;  Pred. No. 1.1e-23;
  Matches   55;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          1 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 58
              |:| |||:||: ||  : || ||  |::     ||  |||| |    ||||| |:| : |
Db          1 QDWLTFQKKHLTNTRDVDCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56

Qy         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104


RESULT 10
AAY28869
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SQ   Sequence 110 AA;

  Query Match             98.5%;  Score 591;  DB 2;  Length 110;
  Best Local Similarity   98.2%;  Pred. No. 7.1e-59;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 NWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVLS 61
              |||||||||||||||||||:|||||||||||||||||||||||||||||||:||||
Db          2 NWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS 61

Qy         62 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110


RESULT 6
AAY28878
ID   AAY28878 standard; protein; 111 AA.
XX
AC   AAY28878;
XX
DT   25-JAN-2000  (first entry)
XX
DE   Recombinant Met(-1) RaCOR1 Gln1Ser amino acid sequence.
XX
KW   Recombinant Met(-1) Rana catesbeiana oocyte ribonuclease Gln1Ser; RaCOR1;
KW   covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
KW   Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
KW   recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;
KW   CD22; RNase; autoimmune disease.
XX
OS   Rana catesbeiana.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
FT                   /note= "Met not found in wild type RaCOR1"
FT   Misc-difference 2
FT                   /note= "Wild type Gln replaced with Ser"
XX
PN   WO9950398-A2.
XX
PD   07-OCT-1999.
XX
PF   26-MAR-1999;   99WO-US006641.
XX
PR   27-MAR-1998;   98US-0079751P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL;
XX
DR   WPI; 1999-610847/52.
DR   N-PSDB; AAZ08135.
XX
PT   New recombinant ribonucleases, used for killing target cells, e.g. for
PT   treating cancers, viral infections or autoimmune diseases.
XX
PS   Claim 22; Page 68; 71pp; English.
XX
CC   The present sequence is a recombinant Rana catesbeiana ribonuclease
CC   (RaCOR1) protein with Met at position 1 and Gln2Ser. Carboxy terminal end
CC   of recombinant RaCOR1 has a covalently bound ligand binding moiety, which
CC   can be a LL2 antibody directed against CD22 on cancerous B cells or human
CC   chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells.
CC   Recombinant ribonucleases can be expressed in bacteria without an N-
CC   terminal methionine due to the presence of a signal peptide that is
CC   cleaved by bacteria. The soluble expression of ribonuclease allows the
CC   proteins to be fused in-frame with ligand binding moieties to form
CC   cytotoxic fusion proteins. They can be used for treatment of cancer and
CC   autoimmune diseases
XX
SQ   Sequence 111 AA;

  Query Match             98.5%;  Score 591;  DB 2;  Length 111;
  Best Local Similarity   98.2%;  Pred. No. 7.1e-59;
  Matches  107;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 NWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVLS 61
              |||||||||||||||||||:|||||||||||||||||||||||||||||||:||||
Db          3 NWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS 62

Qy         62 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111


RESULT 7
AAY33321
ID   AAY33321 standard; protein; 111 AA.
XX
AC   AAY33321;
XX
DT   29-NOV-1999  (first entry)
XX
DE   Frog lectin protein fragment.
XX
KW   Cytotoxic; RNase; ribonuclease; pancreatic; antibody; light chain;
KW   heavy chain; cell surface marker; treatment; tumor; viral infection;
KW   parasite infection; immune dysfunctional cell; autoimmune disease;
KW   contraceptive; cell separation; transplantation; bone marrow ablation;
KW   leukemia cell; T-cell; graft-versus-host disease; bullfrog; lectin.
XX
OS   Rana catesbeiana.
XX
PN   US5955073-A.
XX
PD   21-SEP-1999.
XX
PF   09-JUL-1997;   97US-00891848.
XX
PR   20-APR-1990;   90US-00510696.
PR   22-OCT-1991;   91US-00779195.
PR   04-FEB-1993;   93US-00014082.
PR   22-SEP-1993;   93US-00125462.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL,  Nicholls PJ,  Youle RJ;
XX
DR   WPI; 1999-560488/47.
XX
PT   Recombinantly fused pancreatic RNase-targeting proteins useful for
PT   treating tumors, infections, immune or autoimmune disorders and as a
PT   contraceptive.
XX
PS   Example 3; Fig 19; 47pp; English.
XX
CC   This invention describes a novel nucleic acid construct comprising
CC   sequences encoding functional pancreatic RNase and a second protein
CC   (preferably the light and heavy chains of an antibody) which binds a
CC   specific cell surface marker on a target cell and functions as a
CC   cytotoxic agent. The products can be used for selectively killing cells
CC   expressing a specific surface marker. They can be used for treating
CC   tumors or infected cells (e.g. cells infected by viruses (especially
CC   latent or chronic virus infections, such as human immunodeficiency virus
CC   (HIV)-1, Epstein-Barr virus, herpes viruses (herpes simplex types I and
CC   II), hepatitis viruses (B, non-A-non-B, and delta), herpes zoster,
CC   cytomegalovirus)) and cells infected with parasites (such as the malaria
CC   parasite)). They can also be used for treating immune dysfunctional cells
CC   in immune and autoimmune diseases. Additionally, they may be used as
CC   contraceptives. Finally they can also be used for cell separation in
CC   vitro by selectively killing unwanted types of cells (e.g. in bone
CC   marrow) prior to transplantation into a patient undergoing marrow
CC   ablation by radiation or for killing leukemia cells or T-cells that would
CC   cause graft-versus-host disease. This sequence represents a bullfrog
```

```
CC   N-terminal methionine due to the presence of a signal peptide that is
CC   cleaved by bacteria. The soluble expression of ribonuclease allows the
CC   proteins to be fused in-frame with ligand binding moieties to form
CC   cytotoxic fusion proteins. They can be used for treatment of cancer and
CC   autoimmune diseases
XX
SQ   Sequence 110 AA;

  Query Match             99.3%;  Score 596;  DB 2;  Length 110;
  Best Local Similarity   98.2%;  Pred. No. 1.9e-59;
  Matches  108;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 60
              ||||||||||||||||||||:||||||||||||||||||||||||||||||||:|||
Db          1 QNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 60

Qy         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110


RESULT 4
AAY28873
ID   AAY28873 standard; protein; 111 AA.
XX
AC   AAY28873;
XX
DT   25-JAN-2000  (first entry)
XX
DE   Recombinant Met(-1) RaCOR1.
XX
KW   Recombinant Met(-1) Rana catesbeiana oocyte ribonuclease; RaCOR1; CD22;
KW   covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
KW   Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
KW   recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;
KW   RNase; autoimmune disease.
XX
OS   Rana catesbeiana.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
FT                   /note= "Met not found in wild type RaCOR1"
XX
PN   WO9950398-A2.
XX
PD   07-OCT-1999.
XX
PF   26-MAR-1999;   99WO-US006641.
XX
PR   27-MAR-1998;   98US-0079751P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL;
XX
DR   WPI; 1999-610847/52.
DR   N-PSDB; AAZ08131.
XX
PT   New recombinant ribonucleases, used for killing target cells, e.g. for
PT   treating cancers, viral infections or autoimmune diseases.
XX
PS   Claim 22; Page 63; 71pp; English.
XX
CC   The present sequence is a recombinant Rana catesbeiana oocyte
CC   ribonuclease (RaCOR1) protein with Met at position 1. Carboxy terminal
CC   end of recombinant RaCOR1 has a covalently bound ligand binding moiety,
CC   which can be a LL2 antibody directed against CD22 on cancerous B cells or
CC   human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma
CC   cells. Recombinant ribonucleases can be expressed in bacteria without an
CC   N-terminal methionine due to the presence of a signal peptide that is
CC   cleaved by bacteria. The soluble expression of ribonuclease allows the
CC   proteins to be fused in-frame with ligand binding moieties to form
CC   cytotoxic fusion proteins. They can be used for treatment of cancer and
CC   autoimmune diseases
XX
SQ   Sequence 111 AA;

  Query Match             99.3%;  Score 596;  DB 2;  Length 111;
  Best Local Similarity   98.2%;  Pred. No. 1.9e-59;
  Matches  108;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 60
              ||||||||||||||||||||:||||||||||||||||||||||||||||||||:|||
Db          2 QNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 61

Qy         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111


RESULT 5
AAY28877
ID   AAY28877 standard; protein; 110 AA.
XX
AC   AAY28877;
XX
DT   25-JAN-2000  (first entry)
XX
DE   Recombinant RaCOR1 Gln1Ser amino acid sequence.
XX
KW   Recombinant Rana catesbeiana oocyte ribonuclease; RaCOR1 Gln1Ser; CD22;
KW   covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
KW   bullfrog; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; RNase;
KW   signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
KW   cancer; autoimmune disease.
XX
OS   Rana catesbeiana.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
FT                   /note= "Wild type Gln replaced with Ser"
XX
PN   WO9950398-A2.
XX
PD   07-OCT-1999.
XX
PF   26-MAR-1999;   99WO-US006641.
XX
PR   27-MAR-1998;   98US-0079751P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rybak SM,  Newton DL;
XX
DR   WPI; 1999-610847/52.
DR   N-PSDB; AAZ08134.
XX
PT   New recombinant ribonucleases, used for killing target cells, e.g. for
PT   treating cancers, viral infections or autoimmune diseases.
XX
PS   Claim 22; Page 67; 71pp; English.
XX
CC   The present sequence is a recombinant Rana catesbeiana oocyte
CC   ribonuclease (RaCOR1) protein with Gln1Ser. Carboxy terminal end of
CC   recombinant RaCOR1 has a covalently bound ligand binding moiety, which
CC   can be a LL2 antibody directed against CD22 on cancerous B cells or human
CC   chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells.
CC   Recombinant ribonucleases can be expressed in bacteria without an N-
CC   terminal methionine due to the presence of a signal peptide that is
CC   cleaved by bacteria. The soluble expression of ribonuclease allows the
CC   proteins to be fused in-frame with ligand binding moieties to form
CC   cytotoxic fusion proteins. They can be used for treatment of cancer and
CC   autoimmune diseases
XX
```

CC which can be a LL2 antibody directed against CD22 on cancerous B cells or
CC human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma
CC cells. Recombinant ribonucleases can be expressed in bacteria without an
CC N-terminal methionine due to the presence of a signal peptide that is
CC cleaved by bacteria. The soluble expression of ribonuclease allows the
CC proteins to be fused in-frame with ligand binding moieties to form
CC cytotoxic fusion proteins. They can be used for treatment of cancer and
CC autoimmune diseases
XX
SQ Sequence 110 AA;

Query Match 100.0%; Score 600; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 6.8e-60;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 QNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 60

Qy         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
```

RESULT 2
AAY28876
ID AAY28876 standard; protein; 111 AA.
XX
AC AAY28876;
XX
DT 25-JAN-2000 (first entry)
XX
DE Recombinant Met(-1) RaCOR1 Met22Leu Met57Leu-(His)6 protein.
XX
KW Met(-1) Rana catesbeiana ribonuclease Met22Leu Met57Leu-(His)6; RaCOR1;
KW recombinant; CD22; covalently bound; LL2 antibody; ligand binding moiety;
KW cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG;
KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
KW cancer; bullfrog; RNase; autoimmune disease.
XX
OS Rana catesbeiana.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1
FT /note= "Met not found in wild type RaCOR1"
FT Misc-difference 1
FT /note= "(His)6 histidine tag attached to N-terminal Met"
FT Misc-difference 23
FT /note= "Wild type Met replaced with Leu"
FT Misc-difference 58
FT /note= "Wild type Met replaced with Leu"
XX
PN WO9950398-A2.
XX
PD 07-OCT-1999.
XX
PF 26-MAR-1999; 99WO-US006641.
XX
PR 27-MAR-1998; 98US-0079751P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rybak SM, Newton DL;
XX
DR WPI; 1999-610847/52.
DR N-PSDB; AAZ08133.
XX
PT New recombinant ribonucleases, used for killing target cells, e.g. for
PT treating cancers, viral infections or autoimmune diseases.
XX
PS Claim 22; Page 66; 71pp; English.
XX

CC The present sequence is a recombinant Rana catesbeiana oocyte
CC ribonuclease (RaCOR1) protein with Met at position 1 attached to a (His)6
CC tag, Met23Leu and Met58Leu. Carboxy terminal end of recombinant RaCOR1
CC has a covalently bound ligand binding moiety, which can be a LL2 antibody
CC directed against CD22 on cancerous B cells or human chorionic
CC gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant
CC ribonucleases can be expressed in bacteria without an N-terminal
CC methionine due to the presence of a signal peptide that is cleaved by
CC bacteria. The soluble expression of ribonuclease allows the proteins to
CC be fused in-frame with ligand binding moieties to form cytotoxic fusion
CC proteins. They can be used for treatment of cancer and autoimmune
CC diseases
XX
SQ Sequence 111 AA;

Query Match 100.0%; Score 600; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 6.8e-60;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 QNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 QNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 61

Qy         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
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RESULT 3
AAY28872
ID AAY28872 standard; protein; 110 AA.
XX
AC AAY28872;
XX
DT 25-JAN-2000 (first entry)
XX
DE Rana catesbeiana oocyte ribonuclease (RaCOR1) amino acid sequence.
XX
KW Rana catesbeiana oocyte ribonuclease; RaCOR1; covalently bound; CD22;
KW LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's Sarcoma;
KW human chorionic gonadotrophin; hCG; recombinant ribonuclease; bullfrog;
KW signal peptide; cytotoxic fusion protein; cancer; autoimmune disease;
KW RNase.
XX
OS Rana catesbeiana.
OS Synthetic.
XX
PN WO9950398-A2.
XX
PD 07-OCT-1999.
XX
PF 26-MAR-1999; 99WO-US006641.
XX
PR 27-MAR-1998; 98US-0079751P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rybak SM, Newton DL;
XX
DR WPI; 1999-610847/52.
DR N-PSDB; AAZ08130.
XX
PT New recombinant ribonucleases, used for killing target cells, e.g. for
PT treating cancers, viral infections or autoimmune diseases.
XX
PS Claim 22; Page 62; 71pp; English.
XX
CC The present sequence is a Rana catesbeiana oocyte ribonuclease (RaCOR1)
CC protein encoded by a cDNA modified for expression in E. coli. Carboxy
CC terminal end of RaCOR1 has a covalently bound ligand binding moiety,
CC which can be a LL2 antibody directed against CD22 on cancerous B cells or
CC human chorionic gonadotrophin (hCG) effective against Kaposi's Sarcoma
CC cells. Recombinant ribonucleases can be expressed in bacteria without an

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 7, 2004, 21:25:55 ; Search time 46.9224 Seconds
(without alignments)
662.376 Million cell updates/sec

Title: US-09-961-400-19
Perfect score: 600
Sequence: 1 QNWATFQQKHIINTPIICNT.....ICVKCENQYPVHFAGIGRCP 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	600	100.0	110	2	AAY28874	Aay28874 Recombina
2	600	100.0	111	2	AAY28876	Aay28876 Recombina
3	596	99.3	110	2	AAY28872	Aay28872 Rana cate
4	596	99.3	111	2	AAY28873	Aay28873 Recombina
5	591	98.5	110	2	AAY28877	Aay28877 Recombina
6	591	98.5	111	2	AAY28878	Aay28878 Recombina
7	582.5	97.1	111	2	AAY33321	Aay33321 Frog lect
8	280.5	46.8	104	2	AAW06544	Aaw06544 Antitumou
9	279.5	46.6	104	2	AAY28866	Aay28866 Recombina
10	279.5	46.6	105	2	AAY28869	Aay28869 Recombina
11	277.5	46.2	104	2	AAY28865	Aay28865 Rana pipi
12	277.5	46.2	105	2	AAY28867	Aay28867 Recombina
13	277.5	46.2	127	2	AAY28879	Aay28879 Rana pipi
14	273.5	45.6	104	2	AAW30301	Aaw30301 Recombina
15	273.5	45.6	104	4	AAB31667	Aab31667 Amino aci
16	273.5	45.6	104	4	AAB31666	Aab31666 Amino aci
17	273.5	45.6	104	5	ABG32650	Abg32650 Northern
18	273.5	45.6	104	5	ABG31617	Abg31617 Northern
19	273.5	45.6	105	2	AAY39400	Aay39400 Recombina
20	273.5	45.6	379	2	AAW35126	Aaw35126 R. pipien
21	272.5	45.4	104	2	AAW30302	Aaw30302 Recombina
22	272.5	45.4	104	2	AAY28870	Aay28870 Recombina
23	272.5	45.4	105	2	AAY28871	Aay28871 Recombina
24	270.5	45.1	104	2	AAR12344	Aar12344 Protein w
25	270.5	45.1	104	2	AAR47303	Aar47303 ONCONASE
26	270.5	45.1	104	2	AAW00736	Aaw00736 Protein d
27	270.5	45.1	104	2	AAW14065	Aaw14065 Onconase
28	270.5	45.1	104	2	AAW06543	Aaw06543 Antitumou
29	270.5	45.1	104	2	AAW88233	Aaw88233 Rana pipi
30	270.5	45.1	104	2	AAY33322	Aay33322 Frog onco
31	270.5	45.1	105	2	AAW35123	Aaw35123 R. pipien
32	270.5	45.1	355	2	AAW35125	Aaw35125 R. pipien
33	270.5	45.1	358	2	AAW35130	Aaw35130 R. pipien
34	268.5	44.8	106	2	AAW35122	Aaw35122 R. pipien
35	268.5	44.8	107	2	AAW35117	Aaw35117 R. pipien
36	268.5	44.8	112	2	AAW35118	Aaw35118 R. pipien
37	268.5	44.8	251	2	AAW35134	Aaw35134 R. pipien
38	268.5	44.8	254	2	AAW35135	Aaw35135 R. pipien
39	268.5	44.8	355	2	AAW35133	Aaw35133 R. pipien
40	268.5	44.8	355	2	AAW35129	Aaw35129 R. pipien
41	268.5	44.8	366	2	AAW35132	Aaw35132 R. pipien
42	263.5	43.9	104	2	AAW18224	Aaw18224 Antitumou
43	263.5	43.9	105	2	AAW35115	Aaw35115 R. pipien
44	263.5	43.9	105	2	AAW35116	Aaw35116 R. pipien
45	259.5	43.2	358	2	AAW35127	Aaw35127 R. pipien

ALIGNMENTS

RESULT 1
AAY28874
ID AAY28874 standard; protein; 110 AA.
XX
AC AAY28874;
XX
DT 25-JAN-2000 (first entry)
XX
DE Recombinant RaCOR1 Met22Leu Met57Leu amino acid sequence.
XX
KW Recombinant Rana catesbeiana oocyte ribonuclease; covalently bound;
KW RaCOR1 Met22Leu Met57Leu; LL2 antibody; ligand binding moiety; CD22;
KW cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG;
KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
KW cancer; bullfrog; RNase; autoimmune disease.
XX
OS Rana catesbeiana.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 22
FT /note= "Wild type Met replaced with Leu"
FT Misc-difference 57
FT /note= "Wild type Met replaced with Leu"
XX
PN WO9950398-A2.
XX
PD 07-OCT-1999.
XX
PF 26-MAR-1999; 99WO-US006641.
XX
PR 27-MAR-1998; 98US-0079751P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rybak SM, Newton DL;
XX
DR WPI; 1999-610847/52.
DR N-PSDB; AAZ08132.
XX
PT New recombinant ribonucleases, used for killing target cells, e.g. for
PT treating cancers, viral infections or autoimmune diseases.
XX
PS Claim 22; Page 64; 71pp; English.
XX
CC The present sequence is a recombinant Rana catesbeiana oocyte
CC ribonuclease (RaCOR1) protein with Met22Leu Met57Leu. Carboxy terminal
CC end of recombinant RaCOR1 has a covalently bound ligand binding moiety,

```
RA   Beintema J.J.;
RT   "Secretory ribonuclease genes and pseudogenes in true ruminants.";
RL   Gene 212:259-268(1998).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y11670; CAA72368.1; -.
DR   HSSP; P00656; 1SRN.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT   ACT_SITE     41     41       BY SIMILARITY.
FT   DISULFID     26     84       BY SIMILARITY.
FT   DISULFID     40     95       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID     65     72       BY SIMILARITY.
FT   CARBOHYD     62     62       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   CARBOHYD    129    129       O-LINKED (BY SIMILARITY).
FT   CARBOHYD    133    133       O-LINKED (BY SIMILARITY).
SQ   SEQUENCE   151 AA;  16819 MW;  E95F3757FFC5B233 CRC64;

  Query Match             21.0%;  Score 127.5;  DB 1;  Length 151;
  Best Local Similarity   30.6%;  Pred. No. 8.5e-07;
  Matches   37;  Conservative   17;  Mismatches   44;  Indels   23;  Gaps    7;

Qy          5 ATFQQKHI------INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINM 58
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Db          6 AKFRRQHMDAGSSSSGNSNYCNQMMKRR-RMTHGRCKPVNTFVHESLDSVKAVCS---QK 61

Qy         59 NVL----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHFA 105
              |:          | :   :  |  |   :  | | | :  :  || | || | | ||||
Db         62 NITCKNGQPNCYQSNSTMNITDCRETGSSKYPNCAYKTSQKQKYITVACEGNPYVPVHFD 121

Qy        106 G 106
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Db        122 G 122


Search completed: May  7, 2004, 21:53:06
Job time : 6.60711 secs
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OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Milk, and Serum;
RX   MEDLINE=97409980; PubMed=9266695;
RA   Strydom D.J., Bond M.D., Vallee B.L.;
RT   "An angiogenic protein from bovine serum and milk -- purification and
RT   primary structure of angiogenin-2.";
RL   Eur. J. Biochem. 247:535-544(1997).
CC   -!- FUNCTION: Binds tightly to placental ribonuclease inhibitor and
CC       has very low ribonuclease activity. Has potent angiogenic
CC       activity. Angiogenin induces vascularization of normal and
CC       malignant tissues. Abolishes protein synthesis by specifically
CC       hydrolyzing cellular tRNAs.
CC   -!- TISSUE SPECIFICITY: Serum and milk.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR   HSSP; P10152; 1AGI.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Angiogenesis;
KW   Protein synthesis inhibitor; Glycoprotein;
KW   Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   ACT_SITE     12     12       BY SIMILARITY.
FT   ACT_SITE     39     39       BY SIMILARITY.
FT   ACT_SITE    113    113       BY SIMILARITY.
FT   DISULFID     25     80
FT   DISULFID     38     91
FT   DISULFID     56    106
FT   CARBOHYD     33     33       N-LINKED (GLCNAC. . .).
SQ   SEQUENCE   123 AA;  14522 MW;  B703B9839919FD2F CRC64;

  Query Match             21.0%;  Score 127.5;  DB 1;  Length 123;
  Best Local Similarity   30.6%;  Pred. No. 6.9e-07;
  Matches   33;  Conservative   19;  Mismatches   43;  Indels   13;  Gaps    5;

Qy          7 FQQKHIINTPI-----ICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAIC---TGVINM 58
              | :||   :|        |||:|:     :   ||  ||||  ::  ::|:|     |
Db          8 FLRKHYDPSPTGHDDRYCNTMMERR--NMTRPCKDTNTFIHGNSDDIRAVCDDRNGEPYR 65

Qy         59 NVLSTTR--FQLNTCTRTSITPR-PCPYSSRTETNYICVKCENQYPVH 103
              | |  :|  ||: ||     :|| || | :      | ::| : :|:|
Db         66 NGLRRSRSPFQVTTCRHRGGSPRPPCRYRAFRANRVIVIRCRDGFPIH 113


RESULT 14
RNBR_GIRCA
ID   RNBR_GIRCA     STANDARD;      PRT;   141 AA.
AC   Q29542; Q29533;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ribonuclease, brain (EC 3.1.27.-) (BRB).
GN   BRN.
OS   Giraffa camelopardalis (Giraffe).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Giraffoidea;
OC   Giraffidae; Giraffa.
OX   NCBI_TaxID=9894;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96139017; PubMed=8587129;
RA   Confalone E., Beintema J.J., Sasso M.P., Carsana A., Palmieri M.,
RA   Vento M.T., Furia A.;
RT   "Molecular evolution of genes encoding ribonucleases in ruminant
RT   species.";
RL   J. Mol. Evol. 41:850-858(1995).
RN   [2]
RP   SEQUENCE OF 31-114 FROM N.A.
RX   MEDLINE=93367815; PubMed=8360916;
RA   Breukelman H.J., Beintema J.J., Confalone E., Costanzo C., Sasso M.P.,
RA   Carsana A., Palmieri M., Furia A.;
RT   "Sequences related to the ox pancreatic ribonuclease coding region in
RT   the genomic DNA of mammalian species.";
RL   J. Mol. Evol. 37:29-35(1993).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC   ----------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; S81743; AAB36137.1; -.
DR   EMBL; S65126; AAB27931.1; -.
DR   HSSP; P00656; 2RNS.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT   ACT_SITE     41     41       BY SIMILARITY.
FT   DISULFID     26     84       BY SIMILARITY.
FT   DISULFID     40     95       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID     65     72       BY SIMILARITY.
FT   CARBOHYD     62     62       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   CARBOHYD    129    129       O-LINKED (BY SIMILARITY).
SQ   SEQUENCE   141 AA;  15592 MW;  73745EFE9079591F CRC64;

  Query Match             21.0%;  Score 127.5;  DB 1;  Length 141;
  Best Local Similarity   30.6%;  Pred. No. 7.9e-07;
  Matches   37;  Conservative   17;  Mismatches   44;  Indels   23;  Gaps    7;

Qy          5 ATFQQKHI------INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINM 58
              | |:::|:      :    || :|     :  |:|| ||||:  |   |||:|:
Db          6 AKFRRQHMDSGSSSSSSNSNYCNQMMKRR-RMTHGRCKPVNTFVHESLADVKAVCS---QK 61

Qy         59 NVL----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHFA 105
              |:          | :  :  |  |  :  | | | :  :  || | || | | ||||
Db         62 NITCKNGQPNCYQSNSTMNITDCRETGSSKYPNCAYKTSQKQKYITVACEGNPYVPVHFD 121

Qy        106 G 106
              |
Db        122 G 122


RESULT 15
RNBR_AXIPR
ID   RNBR_AXIPR     STANDARD;      PRT;   151 AA.
AC   P87350;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Ribonuclease, brain (EC 3.1.27.-) (BRB).
GN   BRN.
OS   Axis porcinus (Hog deer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC   Cervidae; Cervinae; Axis.
OX   NCBI_TaxID=57737;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98278842; PubMed=9611269;
RA   Breukelman H.J., van der Munnik N., Kleineidam R.G., Furia A.,
```

```
SQ   SEQUENCE   124 AA;  13804 MW;  0AC28CDE14111845 CRC64;

  Query Match             21.8%;  Score 132.5;  DB 1;  Length 124;
  Best Local Similarity   31.6%;  Pred. No. 2e-07;
  Matches   36;  Conservative   19;  Mismatches   42;  Indels   17;  Gaps    6;

Qy          7 FQQKHI------INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGV-INMN 59
              ||::|:      |:   || :|     :  |:|| ||||:  |   |:|:|: : :|
Db          8 FQRQHMDPDSSSSNSSNYCNLMMSRR-NMTQGRCKPVNTFVHESLADVQAVCSQINVNCK 66

Qy         60 VLSTTRFQLNT------CTRTSITPRP-CPYSSRTETNYICVKCENQ--YPVHF 104
                | :| |:      | :|  :  | | | :  |  :| | ||     ||||
Db         67 NGQTNCYQSNSTMHITDCRQTGSSKYPNCAYKASQEQKHIIVACEGNPPVPVHF 120


RESULT 11
RNP_IGUIG
ID   RNP_IGUIG      STANDARD;      PRT;   119 AA.
AC   P80287;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
OS   Iguana iguana (Common iguana).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.
OX   NCBI_TaxID=8517;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Pancreas;
RX   MEDLINE=94139745; PubMed=8307028;
RA   Zhao W., Beintema J.J., Hofsteenge J.;
RT   "The amino acid sequence of iguana (Iguana iguana) pancreatic
RT   ribonuclease.";
RL   Eur. J. Biochem. 219:641-646(1994).
CC   -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC       phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC       with 2',3'-cyclic phosphate intermediates.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Pancreas.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR   PIR; S41111; S41111.
DR   HSSP; P00656; 1LSQ.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Pyrrolidone carboxylic acid.
FT   MOD_RES      1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID     25     80      BY SIMILARITY.
FT   DISULFID     39     91      BY SIMILARITY.
FT   DISULFID     57    106      BY SIMILARITY.
FT   ACT_SITE     10     10      BY SIMILARITY.
FT   ACT_SITE     40     40      BY SIMILARITY.
FT   ACT_SITE    113    113      BY SIMILARITY.
SQ   SEQUENCE   119 AA;  13324 MW;  6072FB5B7B15BD5A CRC64;

  Query Match             21.7%;  Score 131.5;  DB 1;  Length 119;
  Best Local Similarity   30.4%;  Pred. No. 2.5e-07;
  Matches   35;  Conservative   16;  Mismatches   51;  Indels   13;  Gaps    4;

Qy          2 QNWATFQQKHI-------INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAIC-- 52
              |:|::|| |||        |    |: :|     :   :||  |||: :| : :: :|
Db          1 QDWSSFQNKHIDYPETSASNPNAYCDLMMQRR-NLNPTKCKTRNTFVHASPSEIQQVCGS 59

Qy         53 --TGVINMNVLSTTRFQLNTCTRTSIT-PRPCPYSSRTETNYICVKCENQYPVHF 104
                |   :  |  | | |     | |  | |:    |  | : |||  ||||
Db         60 GGTHYEDNLYDSNESFDLTDCKNVGGTAPSSCKYNGTPGTKRIRIACENNQPVHF 114


RESULT 12
RNBR_CAPCA
ID   RNBR_CAPCA     STANDARD;      PRT;   151 AA.
AC   P79351;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Ribonuclease, brain (EC 3.1.27.-) (BRB).
OS   Capreolus capreolus (Roe deer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC   Cervidae; Odocoileinae; Capreolus.
OX   NCBI_TaxID=9858;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98278842; PubMed=9611269;
RA   Breukelman H.J., van der Munnik N., Kleineidam R.G., Furia A.,
RA   Beintema J.J.;
RT   "Secretory ribonuclease genes and pseudogenes in true ruminants.";
RL   Gene 212:259-268(1998).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; Y11673; CAA72371.1; -.
DR   HSSP; P00656; 1SRN.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT   ACT_SITE     41     41      BY SIMILARITY.
FT   DISULFID     26     84      BY SIMILARITY.
FT   DISULFID     40     95      BY SIMILARITY.
FT   DISULFID     58    110      BY SIMILARITY.
FT   DISULFID     65     72      BY SIMILARITY.
FT   CARBOHYD     62     62      N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT   CARBOHYD    129    129      O-LINKED (BY SIMILARITY).
FT   CARBOHYD    133    133      O-LINKED (BY SIMILARITY).
SQ   SEQUENCE   151 AA;  16971 MW;  392D0E6302F006A6 CRC64;

  Query Match             21.2%;  Score 128.5;  DB 1;  Length 151;
  Best Local Similarity   29.4%;  Pred. No. 6.6e-07;
  Matches   35;  Conservative   17;  Mismatches   44;  Indels   23;  Gaps    6;

Qy          5 ATFQQKHI------INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINM 58
              | |:::|:      |   || :|     :  |:|| ||||:  |   |||:|:
Db          6 AKFRRQHMDSGSSSSGNPNYCNQMMKRR-RMTHGRCKPVNTFVHESLDNVKAVCS---QK 61

Qy         59 NVL----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCENQ--YPVHF 104
              |:          | :   :  | :|  :  | | | :  :  || | ||     ||||
Db         62 NITCKNGQPNCYQSNSTMNITDCRQTGSSKYPNCAYKTSQKQKYITVACEGDPYVPVHF 120


RESULT 13
ANG2_BOVIN
ID   ANG2_BOVIN     STANDARD;      PRT;   123 AA.
AC   P80929;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Angiogenin-2 (EC 3.1.27.-).
GN   ANG2.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Ribonuclease, brain precursor (EC 3.1.27.-) (BRB).
GN   BRN.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92093604; PubMed=1754384;
RA   Sasso M.P., Carsana A., Confalone E., Cosi C., Sorrentino S.,
RA   Viola M., Palmieri M., Russo E., Furia A.;
RT   "Molecular cloning of the gene encoding the bovine brain ribonuclease
RT   and its expression in different regions of the brain.";
RL   Nucleic Acids Res. 19:6469-6474(1991).
RN   [2]
RP   SEQUENCE OF 27-167, AND CARBOHYDRATE-LINKAGE SITES.
RC   TISSUE=Brain;
RX   MEDLINE=89214015; PubMed=3243767;
RA   Watanabe H., Katoh H., Ishii M., Komoda Y., Sanda A., Takizawa Y.,
RA   Ohgi K., Irie M.;
RT   "Primary structure of a ribonuclease from bovine brain.";
RL   J. Biochem. 104:939-945(1988).
RN   [3]
RP   SEQUENCE OF 27-167 FROM N.A.
RX   MEDLINE=96139017; PubMed=8587129;
RA   Confalone E., Beintema J.J., Sasso M.P., Carsana A., Palmieri M.,
RA   Vento M.T., Furia A.;
RT   "Molecular evolution of genes encoding ribonucleases in ruminant
RT   species.";
RL   J. Mol. Evol. 41:850-858(1995).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC   ---------------------------------------------------------------------
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X59767; CAA42439.1; -.
DR   EMBL; S81744; AAB36138.1; -.
DR   PIR; S20066; S20066.
DR   HSSP; P00656; 2RNS.
DR   GlycoSuiteDB; P39873; -.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Glycoprotein; Signal.
FT   SIGNAL       1     26
FT   CHAIN       27    167       RIBONUCLEASE, BRAIN.
FT   ACT_SITE    38     38       BY SIMILARITY.
FT   ACT_SITE    67     67       BY SIMILARITY.
FT   ACT_SITE   145    145       BY SIMILARITY.
FT   DISULFID    52    110       BY SIMILARITY.
FT   DISULFID    66    121       BY SIMILARITY.
FT   DISULFID    84    136       BY SIMILARITY.
FT   DISULFID    91     98       BY SIMILARITY.
FT   CARBOHYD    88     88       N-LINKED (GLCNAC. . .).
FT                               /FTId=CAR_000005.
FT   CARBOHYD   155    155       O-LINKED.
FT   CARBOHYD   159    159       O-LINKED.
FT   CONFLICT   155    155       T -> S (IN REF. 2).
SQ   SEQUENCE   167 AA;  18450 MW;  681CAAC3CC2FC459 CRC64;

  Query Match             22.0%;  Score 133.5;  DB 1;  Length 167;
  Best Local Similarity   31.4%;  Pred. No. 2.1e-07;

  Matches   38;  Conservative   17;  Mismatches   43;  Indels   23;  Gaps    7;

Qy          5 ATFQQKHI------INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINM 58
              | |:::|:       : |  || :|     :  |:|| |||:  |   |||:|:
Db         32 AKFRRQHMDSGSSSSSNPNYCNQMMKRR-RMTHGRCKPVNTFVHESLDDVKAVCS---QK 87

Qy         59 NVL----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHFA 105
              |:          |  :  :|  |  :  | | |  :  :  || | || | | ||||
Db         88 NITCKNGHPNCYQSKSTMSITDCRETGSSKYPNCAYKTSQKQKYITVACEGNPYVPVHFD 147

Qy        106 G 106
              |
Db        148 G 148


RESULT 10
RNP_PIG
ID   RNP_PIG        STANDARD;      PRT;   124 AA.
AC   P00671;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
GN   RNASE1 OR RNS1.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=70104197; PubMed=5460946;
RA   Jackson R.L., Hirs C.H.W.;
RT   "The primary structure of porcine pancreatic ribonuclease. II. The
RT   amino acid sequence of the reduced S-aminoethylated protein.";
RL   J. Biol. Chem. 245:637-653(1970).
RN   [2]
RP   REVISION TO 2.
RA   Wierenga R.K., Huizinga J.D., Gaastra W., Welling G.W., Beintema J.J.;
RT   "Affinity chromatography of porcine pancreatic ribonuclease and
RT   reinvestigation of the N-terminal amino acid sequence.";
RL   FEBS Lett. 31:181-185(1973).
RN   [3]
RP   DISULFIDE BONDS.
RX   MEDLINE=70104198; PubMed=4904878;
RA   Phelan J.J., Hirs C.H.W.;
RT   "The primary structure of porcine pancreatic ribonuclease. 3. The
RT   disulfide bonds.";
RL   J. Biol. Chem. 245:654-661(1970).
CC   -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC       phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC       with 2',3'-cyclic phosphate intermediates.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Pancreas.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR   PIR; A92071; NRPG.
DR   HSSP; P00656; 1SRN.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT   DISULFID     26     84
FT   DISULFID     40     95
FT   DISULFID     58    110
FT   DISULFID     65     72
FT   ACT_SITE     12     12       BY SIMILARITY.
FT   ACT_SITE     41     41       BY SIMILARITY.
FT   ACT_SITE    119    119       BY SIMILARITY.
FT   CARBOHYD     21     21       N-LINKED (GLCNAC. . .).
FT   CARBOHYD     34     34       N-LINKED (GLCNAC. . .).
FT   CARBOHYD     76     76       N-LINKED (GLCNAC. . .).
```

```
DR   PIR; A00818; NRWHK.
DR   HSSP; P00656; 1SRN.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT   DISULFID     26     84       BY SIMILARITY.
FT   DISULFID     40     95       BY SIMILARITY.
FT   DISULFID     58    110       BY SIMILARITY.
FT   DISULFID     65     72       BY SIMILARITY.
FT   ACT_SITE     12     12       BY SIMILARITY.
FT   ACT_SITE     41     41       BY SIMILARITY.
FT   ACT_SITE    119    119       BY SIMILARITY.
FT   CARBOHYD     76     76       N-LINKED (GLCNAC. . .) (30%).
SQ   SEQUENCE   124 AA;  14125 MW;  F57475459F697E20 CRC64;

  Query Match             22.3%;  Score 135.5;  DB 1;  Length 124;
  Best Local Similarity   33.3%;  Pred. No. 9.5e-08;
  Matches   39;  Conservative   16;  Mismatches   39;  Indels   23;  Gaps    7;

Qy          7 FQQKHII------NTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60
              ||::|:        | |  || :|     :  |:|| ||||:  |   |||:|:     ||
Db          8 FQRQHMDSGNSPGNNPNYCNQMMMRR-KMTQGRCKPVNTFVHESLEDVKAVCS---QKNV 63

Qy         61 L----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 104
              |          | :   :  | :|  :  | | |  :  :  :| | || | | ||||
Db         64 LCKNGRTNCYESNSTMHITDCRQTGSSKYPNCAYKTSQKEKHIIVACEGNPYVPVHF 120


RESULT 8
ANGI_MOUSE
ID   ANGI_MOUSE     STANDARD;      PRT;   145 AA.
AC   P21570;
DT   01-MAY-1991 (Rel. 18, Created)
DT   01-MAY-1991 (Rel. 18, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).
GN   ANG.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91025023; PubMed=2222458;
RA   Bond M.D., Vallee B.L.;
RT   "Isolation and sequencing of mouse angiogenin DNA.";
RL   Biochem. Biophys. Res. Commun. 171:988-995(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FVB/N; TISSUE=Liver;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   PARTIAL SEQUENCE.
RC   TISSUE=Serum;
RX   MEDLINE=93192291; PubMed=8448182;
RA   Bond M.D., Strydom D.J., Vallee B.L.;
RT   "Characterization and sequencing of rabbit, pig and mouse
RT   angiogenins: discernment of functionally important residues and
RT   regions.";
RL   Biochim. Biophys. Acta 1162:177-186(1993).
CC   -!- FUNCTION: May function as a tRNA-specific ribonuclease that binds
CC       to actin on the surface of endothelial cells; once bound,
CC       angiogenin is endocytosed and translocated to the nucleus, thereby
CC       promoting the endothelial invasiveness necessary for blood vessel
CC       formation. Angiogenin induces vascularization of normal and
CC       malignant tissues. Abolishes protein synthesis by specifically
CC       hydrolyzing cellular tRNAs.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U22516; AAA91366.1; -.
DR   EMBL; BC055355; AAH55355.1; -.
DR   PIR; A35932; A35932.
DR   HSSP; P03950; 1A4Y.
DR   MGD; MGI:88022; Ang.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Angiogenesis;
KW   Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
FT   SIGNAL        1     24
FT   CHAIN        25    145       ANGIOGENIN.
FT   MOD_RES      25     25       PYRROLIDONE CARBOXYLIC ACID (BY
FT                                SIMILARITY).
FT   ACT_SITE     37     37       BY SIMILARITY.
FT   ACT_SITE     64     64       BY SIMILARITY.
FT   ACT_SITE    137    137       BY SIMILARITY.
FT   DISULFID     50    104       BY SIMILARITY.
FT   DISULFID     63    115       BY SIMILARITY.
FT   DISULFID     81    130       BY SIMILARITY.
SQ   SEQUENCE   145 AA;  16228 MW;  06944260BB764938 CRC64;

  Query Match             22.3%;  Score 135.5;  DB 1;  Length 145;
  Best Local Similarity   39.5%;  Pred. No. 1.1e-07;
  Matches   30;  Conservative   12;  Mismatches   29;  Indels    5;  Gaps    3;

Qy         34 CKRVNTFIISSATTVKAIC---TGVINMNV-LSTTRFQLNTCTRTSITPR-PCPYSSRTE 88
              || |||||  : : :||||         |: :| : ||: ||  |  :|| || | :
Db         63 CKDVNTFIHGNKSNIKAICGANGSPYRENLRMSKSPFQVTTCKHTGGSPRPPCQYRASAG 122

Qy         89 TNYICVKCENQYPVHF 104
                :: : |||  ||||
Db        123 FRHVVIACENGLPVHF 138


RESULT 9
RNBR_BOVIN
ID   RNBR_BOVIN     STANDARD;      PRT;   167 AA.
AC   P39873;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
```

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RT   developmentally regulated genes when expressed in NIH 3T3
RT   fibroblasts.";
RL   Mol. Cell. Biol. 17:1503-1512(1997).
CC   -!- FUNCTION: Angiogenin induces vascularization of normal and
CC       malignant tissues. Abolishes protein synthesis by specifically
CC       hydrolyzing cellular tRNAs (By similarity).
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U72672; AAC05794.1; -.
DR   HSSP; P10152; 1AGI.
DR   MGD; MGI:1201793; Angl.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Angiogenesis;
KW   Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
FT   SIGNAL        1     24       POTENTIAL.
FT   CHAIN        25    145       ANGIOGENIN-3.
FT   MOD_RES      25     25       PYRROLIDONE CARBOXYLIC ACID
FT                                (BY SIMILARITY).
FT   ACT_SITE     37     37       BY SIMILARITY.
FT   ACT_SITE     64     64       BY SIMILARITY.
FT   ACT_SITE    137    137       BY SIMILARITY.
FT   DISULFID     50    104       BY SIMILARITY.
FT   DISULFID     63    115       BY SIMILARITY.
FT   DISULFID     81    130       BY SIMILARITY.
SQ   SEQUENCE   145 AA;  16696 MW;  DE9D3BC92F1D682C CRC64;

  Query Match             25.5%;  Score 154.5;  DB 1;  Length 145;
  Best Local Similarity   43.6%;  Pred. No. 1e-09;
  Matches   34;  Conservative   12;  Mismatches   23;  Indels    9;  Gaps    4;

Qy         34 CKRVNTFIISSATTVKAIC------TGVINMNVLSTTRFQLNTCTRTSITPR-PCPYSSR 86
              || |||||  :   :||||       || |  : | :|||: |||    :|| || |:: 
Db         63 CKEVNTFIHDTKNNIKAICGENGRPYGV-NFRI-SNSRFQVTTCTHKGGSPRPPCQYNAF 120

Qy         87 TETNYICVKCENQYPVHF 104
                :  || : ||: :|||| 
Db        121 KDFRYIVIACEDGWPVHF 138


RESULT 6
ANGR_MOUSE
ID   ANGR_MOUSE     STANDARD;      PRT;   145 AA.
AC   Q64438;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Angiogenin-related protein precursor.
GN   ANGRP.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129; TISSUE=Liver;
RX   MEDLINE=96079109; PubMed=8530072;
RA   Brown W.E., Nobile V., Subramanian V., Shapiro R.;
RT   "The mouse angiogenin gene family: structures of an angiogenin-related
RT   protein gene and two pseudogenes.";
RL   Genomics 29:200-206(1995).
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U22519; AAA91367.1; -.
DR   HSSP; P03950; 1A4Y.
DR   MGD; MGI:104984; Angrp.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Signal; Hydrolase; Nuclease; Endonuclease;
KW   Pyrrolidone carboxylic acid.
FT   SIGNAL        1     24       POTENTIAL.
FT   CHAIN        25    145       ANGIOGENIN-RELATED PROTEIN.
FT   MOD_RES      25     25       PYRROLIDONE CARBOXYLIC ACID (BY
FT                                SIMILARITY).
FT   ACT_SITE     37     37       BY SIMILARITY.
FT   ACT_SITE     64     64       BY SIMILARITY.
FT   ACT_SITE    137    137       BY SIMILARITY.
FT   DISULFID     50    104       BY SIMILARITY.
FT   DISULFID     63    115       BY SIMILARITY.
FT   DISULFID     81    130       BY SIMILARITY.
SQ   SEQUENCE   145 AA;  16612 MW;  29A6EB814429C4AD CRC64;

  Query Match             24.6%;  Score 149.5;  DB 1;  Length 145;
  Best Local Similarity   43.4%;  Pred. No. 3.5e-09;
  Matches   33;  Conservative   10;  Mismatches   28;  Indels    5;  Gaps    3;

Qy         34 CKRVNTFIISSATTVKAIC---TGVINMNV-LSTTRFQLNTCTRTSITPR-PCPYSSRTE 88
              || |||||  :   :||||         |: :| :|||: |||    :|| || | :  
Db         63 CKDVNTFIHDTKNNIKAICGKKGSPYGRNLRISKSRFQVTTCTHKGRSPRPPCRYRASKG 122

Qy         89 TNYICVKCENQYPVHF 104
                || : ||| :|||| 
Db        123 FRYIIIGCENGWPVHF 138


RESULT 7
RNP_BALAC
ID   RNP_BALAC     STANDARD;      PRT;   124 AA.
AC   P00673;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
GN   RNASE1 OR RNS1.
OS   Balaenoptera acutorostrata (Minke whale) (Lesser rorqual).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
OC   Balaenopteridae; Balaenoptera.
OX   NCBI_TaxID=9767;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76277855; PubMed=962870;
RA   Emmens M., Welling G.W., Beintema J.J.;
RT   "The amino acid sequence of pike-whale (lesser-rorqual) pancreatic
RT   ribonuclease.";
RL   Biochem. J. 157:317-323(1976).
CC   -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC       phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC       with 2',3'-cyclic phosphate intermediates.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Pancreas.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
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RL   J. Biochem. 106:729-735(1989).
CC   -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC       phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC       with 2',3'-cyclic phosphate intermediates.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR   PIR; JX0085; JX0085.
DR   HSSP; P11916; 1BC4.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Pyrrolidone carboxylic acid.
FT   MOD_RES      1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   ACT_SITE     10     10      BY SIMILARITY.
FT   ACT_SITE     35     35      BY SIMILARITY.
FT   ACT_SITE     104    104     BY SIMILARITY.
FT   DISULFID     19     72      BY SIMILARITY.
FT   DISULFID     34     82      BY SIMILARITY.
FT   DISULFID     52     97      BY SIMILARITY.
FT   DISULFID     94     111     PROBABLE.
SQ   SEQUENCE   111 AA;  12461 MW;  D64BA72456C10788 CRC64;

  Query Match             61.6%;  Score 374;  DB 1;  Length 111;
  Best Local Similarity   65.8%;  Pred. No. 1.9e-33;
  Matches   73;  Conservative    9;  Mismatches   27;  Indels    2;  Gaps    2;

Qy          2 QNWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 59
              |||| |::||| :|  | |||||| ||||||:|| |||||||   |||||:||  :
Db          1 QNWAKFKEKHIRSTSSIDCNTIMDKAIYIVGGKCKERNTFIISSEDNVKAICSGVSPDRK 60

Qy         60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
               |||| |:|||| | |||||||||    : | |||||| | |||| |||:|
Db         61 ELSTTSFKLNTCIRDSITPRPCPYHPSPDNNKICVKCEKQLPVHFVGIGKC 111


RESULT 4
RN30_RANPI
ID   RN30_RANPI     STANDARD;      PRT;   104 AA.
AC   P22069;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   P-30 protein (EC 3.1.27.-) (Onconase).
OS   Rana pipiens (Northern leopard frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8404;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Embryo;
RX   MEDLINE=91093131; PubMed=1985896;
RA   Ardelt W., Mikulski S.M., Shogen K.;
RT   "Amino acid sequence of an anti-tumor protein from Rana pipiens
RT   oocytes and early embryos. Homology to pancreatic ribonucleases.";
RL   J. Biol. Chem. 266:245-251(1991).
RN   [2]
RP   3D-STRUCTURE MODELING.
RX   MEDLINE=93066156; PubMed=1438177;
RA   Mosimann S.C., Johns K.L., Ardelt W., Mikulski S.M., Shogen K.,
RA   James M.N.G.;
RT   "Comparative molecular modeling and crystallization of P-30 protein:
RT   a novel antitumor protein of Rana pipiens oocytes and early
RT   embryos.";
RL   Proteins 14:392-400(1992).
RN   [3]
RP   X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
RX   MEDLINE=94166079; PubMed=8120892;
RA   Mosimann S.C., Ardelt W., James M.N.G.;
RT   "Refined 1.7 A X-ray crystallographic structure of P-30 protein, an
RT   amphibian ribonuclease with anti-tumor activity.";
RL   J. Mol. Biol. 236:1141-1153(1994).
CC   -!- FUNCTION: Basic protein with antiproliferative/cytotoxic activity
CC       against several tumor cell lines in vitro, as well as antitumor
CC       in vivo. It exhibits a ribonuclease-like activity against high
CC       molecular weight ribosomal RNA.
CC   -!- DEVELOPMENTAL STAGE: Early embryos (up to four blastomere stage).
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR   PDB; 1ONC; 31-JAN-94.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; 3D-structure;
KW   Pyrrolidone carboxylic acid.
FT   MOD_RES      1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   ACT_SITE     10     10
FT   ACT_SITE     31     31
FT   ACT_SITE     97     97
FT   DISULFID     19     68
FT   DISULFID     30     75
FT   DISULFID     48     90
FT   DISULFID     87     104
FT   HELIX        3      10
FT   STRAND       11     12
FT   HELIX        19     22
FT   TURN         23     24
FT   TURN         26     30
FT   STRAND       33     38
FT   HELIX        41     45
FT   HELIX        46     48
FT   TURN         49     50
FT   STRAND       55     58
FT   STRAND       63     70
FT   TURN         74     75
FT   STRAND       77     84
FT   STRAND       86     91
FT   TURN         92     93
FT   STRAND       94     101
SQ   SEQUENCE   104 AA;  11845 MW;  22A753C2F9E566B4 CRC64;

  Query Match             45.7%;  Score 277.5;  DB 1;  Length 104;
  Best Local Similarity   49.5%;  Pred. No. 4.2e-23;
  Matches   55;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          2 QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 59
              |:| |||:||| ||  : |: ||  |::     ||  |||| |    ||||| |:| : |
Db          1 QDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56

Qy         60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104


RESULT 5
ANG3_MOUSE
ID   ANG3_MOUSE     STANDARD;      PRT;   145 AA.
AC   P97802;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Angiogenin-3 precursor (EC 3.1.27.-) (Angiogenin-related protein 2)
DE   (EF-5).
GN   ANG3 OR ANGL.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RX   MEDLINE=97184476; PubMed=9032278;
RA   Fu X., Kamps M.P.;
RT   "E2a-Pbx1 induces aberrant expression of tissue-specific and
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CC       residues with a 3'flanking guanine. Hydrolyzes poly(U) and poly(C)
CC       as substrates, and prefers the former. The S-lectins in frog eggs
CC       may be involved in the fertilization and development of the frog
CC       embryo. This lectin agglutinates various animal cells, including
CC       normal lymphocytes, erythrocytes, and fibroblasts of animal and
CC       human origin. It is cytotoxic against several tumor cells.
CC   -!- SUBUNIT: Monomer.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF039104; AAD10702.1; -.
DR   PIR; A27121; A27121.
DR   PDB; 1BC4; 28-OCT-98.
DR   PDB; 1M07; 21-JAN-03.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure;
KW   Signal; Pyrrolidone carboxylic acid.
FT   SIGNAL        1     22
FT   CHAIN        23    133       RIBONUCLEASE, OOCYTES.
FT   MOD_RES      23     23       PYRROLIDONE CARBOXYLIC ACID.
FT   ACT_SITE     32     32
FT   ACT_SITE     57     57
FT   ACT_SITE    125    125
FT   DISULFID     41     93
FT   DISULFID     56    103
FT   DISULFID     74    118
FT   DISULFID    115    132
FT   HELIX        25     32
FT   HELIX        41     45
FT   TURN         48     49
FT   STRAND       59     63
FT   HELIX        67     73
FT   TURN         74     74
FT   STRAND       79     84
FT   STRAND       90     95
FT   STRAND      105    110
FT   STRAND      114    119
FT   TURN        120    121
FT   STRAND      122    129
SQ   SEQUENCE   133 AA;  14762 MW;  A7D62594F7D16F0C CRC64;

  Query Match             97.4%;  Score 591.5;  DB 1;  Length 133;
  Best Local Similarity   99.1%;  Pred. No. 9.4e-57;
  Matches  110;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          2 QNWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db         23 QNWATFQQKHIINTPIINCNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 82

Qy         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 133


RESULT 2
LECS_RANJA
ID   LECS_RANJA     STANDARD;      PRT;   111 AA.
AC   P18839;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Sialic acid-binding lectin (EC 3.1.27.-).
OS   Rana japonica (Japanese reddish frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8402;
RN   [1]
RP   SEQUENCE, AND DISULFIDE BONDS.
RC   TISSUE=Egg;
RX   MEDLINE=91035319; PubMed=2229005;
RA   Kamiya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawauchi H.,
RA   Takayanagi Y., Titani K.;
RT   "Amino acid sequence of a lectin from Japanese frog (Rana japonica)
RT   eggs.";
RL   J. Biochem. 108:139-143(1990).
CC   -!- FUNCTION: The S-lectins in frog eggs may be involved in the
CC       fertilization and development of the frog embryo. This lectin
CC       preferentially agglutinate a large variety of tumor cells, but it
CC       does not agglutinate non-transformed cells and erythrocytes.
CC   -!- SUBUNIT: Monomer.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR   PIR; JX0120; JX0120.
DR   HSSP; P11916; 1BC4.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNAse_Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin;
KW   Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   ACT_SITE     10     10       BY SIMILARITY.
FT   ACT_SITE     35     35       BY SIMILARITY.
FT   ACT_SITE    104    104       BY SIMILARITY.
FT   DISULFID     19     72
FT   DISULFID     34     82
FT   DISULFID     52     97
FT   DISULFID     94    111
SQ   SEQUENCE   111 AA;  12326 MW;  FDEBDDF3834ED679 CRC64;

  Query Match             75.0%;  Score 455;  DB 1;  Length 111;
  Best Local Similarity   78.4%;  Pred. No. 3.7e-42;
  Matches   87;  Conservative    7;  Mismatches   15;  Indels    2;  Gaps    2;

Qy          2 QNWATFQQKHIINTP-IICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGV-INMN 59
              |||| ||:||| ||  | ||||||  :|||||||||  |||||||||||||||:|   | |
Db          1 QNWAKFQEKHIPNTSNINCNTIMDKSIYIVGGQCKERNTFIISSATTVKAICSGASTNRN 60

Qy         60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              |||||||||||| |::  ||||||:|||||| |||||||: ||||||||||
Db         61 VLSTTRFQLNTCIRSATAPRPCPYNSRTETNVICVKCENRLPVHFAGIGRC 111


RESULT 3
RNPL_RANCA
ID   RNPL_RANCA     STANDARD;      PRT;   111 AA.
AC   P14626;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Ribonuclease, liver (EC 3.1.27.5).
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Liver;
RX   MEDLINE=90130374; PubMed=2613682;
RA   Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,
RA   Okazaki T., Ohgi K., Irie M.;
RT   "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana)
RT   liver.";
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 7, 2004, 21:30:40 ; Search time 5.60711 Seconds
(without alignments)
1030.796 Million cell updates/sec

Title: US-09-961-400-17
Perfect score: 607
Sequence: 1 MQNWATFQQKHIINTPIICN.....ICVKCENQYPVHFAGIGRCP 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	591.5	97.4	133	1	RNPO_RANCA	P11916 rana catesb
2	455	75.0	111	1	LECS_RANJA	P18839 rana japoni
3	374	61.6	111	1	RNPL_RANCA	P14626 rana catesb
4	277.5	45.7	104	1	RN30_RANPI	P22069 rana pipien
5	154.5	25.5	145	1	ANG3_MOUSE	P97802 mus musculu
6	149.5	24.6	145	1	ANGR_MOUSE	Q64438 mus musculu
7	135.5	22.3	124	1	RNP_BALAC	P00673 balaenopter
8	135.5	22.3	145	1	ANGI_MOUSE	P21570 mus musculu
9	133.5	22.0	167	1	RNBR_BOVIN	P39873 bos taurus
10	132.5	21.8	124	1	RNP_PIG	P00671 sus scrofa
11	131.5	21.7	119	1	RNP_IGUIG	P80287 iguana igua
12	128.5	21.2	151	1	RNBR_CAPCA	P79351 capreolus c
13	127.5	21.0	123	1	ANG2_BOVIN	P80929 bos taurus
14	127.5	21.0	141	1	RNBR_GIRCA	Q29542 giraffa cam
15	127.5	21.0	151	1	RNBR_AXIPR	P87350 axis porcin
16	125	20.6	146	1	ANGI_SAISC	Q8wn60 saimiri sci
17	124	20.4	146	1	ANGI_MIOTA	Q8wn65 miopithecus
18	123.5	20.3	143	1	RNBR_SHEEP	Q29543 ovis aries
19	122.5	20.2	124	1	RNP_ANTAM	P00668 antilocapra
20	122.5	20.2	146	1	ANGI_CERAE	Q8wn66 cercopithec
21	122	20.1	122	1	RNP_MACRU	P00686 macropus ru
22	120.5	19.9	128	1	RNP_MYOCO	P00676 myocastor c
23	120.5	19.9	149	1	RNP_MOUSE	P00683 mus musculu
24	120	19.8	146	1	ANGI_AOTTR	Q8wn61 aotus trivi
25	120	19.8	147	1	ANGI_PONPY	Q8wn67 pongo pygma
26	119.5	19.7	123	1	ANGI_PIG	P31346 sus scrofa
27	118.5	19.5	128	1	RNPB_CAVPO	P00679 cavia porce
28	118	19.4	146	1	ANGI_SAGOE	Q8wn62 saguinus oe
29	117.5	19.4	128	1	RNP_HORSE	P00674 equus cabal
30	116.5	19.2	124	1	RNP_CAMDR	P00670 camelus dro
31	116.5	19.2	128	1	RNP_PROGU	P04059 proechimys
32	115.5	19.0	119	1	RNS4_BOVIN	P15467 bos taurus
33	115.5	19.0	146	1	ANGI_MACMU	Q8wn63 macaca mula
34	114	18.8	148	1	ANGI_BOVIN	P10152 bos taurus
35	113.5	18.7	124	1	RNP_RANTA	P00666 rangifer ta
36	113.5	18.7	146	1	ANGI_PAPHA	Q8wn64 papio hamad
37	113	18.6	147	1	ANGI_HUMAN	P03950 homo sapien
38	113	18.6	147	1	ANGI_PANTR	Q8wme8 pan troglod
39	112.5	18.5	124	1	RNP_CAPCA	P00664 capreolus c
40	112.5	18.5	124	1	RNP_GIRCA	P00662 giraffa cam
41	112.5	18.5	148	1	RNS4_MOUSE	Q9jjh1 mus musculu
42	112	18.5	125	1	ANGI_RABIT	P31347 oryctolagus
43	111.5	18.4	130	1	RNP_CRILO	P24717 cricetulus
44	111.5	18.4	147	1	RNS4_RAT	O55004 rattus norv
45	111.5	18.4	149	1	RNP_ACOCA	Q9wtt5 acomys cahi

ALIGNMENTS

RESULT 1
RNPO_RANCA
ID RNPO_RANCA STANDARD; PRT; 133 AA.
AC P11916; Q9PWR7;
DT 01-OCT-1989 (Rel. 12, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ribonuclease, oocytes precursor (EC 3.1.27.-) (RC-RNase) (Sialic acid-
DE binding lectin) (SBL-C).
GN RCR.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98165825; PubMed=9497370;
RA Huang H.C., Wang S.C., Leu Y.J., Lu S.C., Liao Y.D.;
RT "The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease.
RT Tissue distribution, cloning, purification, cytotoxicity, and active
RT residues for RNase activity.";
RL J. Biol. Chem. 273:6395-6401(1998).
RN [2]
RP SEQUENCE OF 23-133.
RC TISSUE=Egg;
RX MEDLINE=87299649; PubMed=3304421;
RA Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H.,
RA Takayanagi G., Hakomori S.;
RT "Amino acid sequence of sialic acid binding lectin from frog (Rana
RT catesbeiana) eggs.";
RL Biochemistry 26:2189-2194(1987).
RN [3]
RP CHARACTERIZATION, AND SEQUENCE OF 81-101.
RX MEDLINE=92220613; PubMed=1373237;
RA Liao Y.-D.;
RT "A pyrimidine-guanine sequence-specific ribonuclease from Rana
RT catesbeiana (bullfrog) oocytes.";
RL Nucleic Acids Res. 20:1371-1377(1992).
RN [4]
RP CHARACTERIZATION.
RC TISSUE=Egg;
RX MEDLINE=93192604; PubMed=8448385;
RA Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawauchi H.,
RA Takayanagi Y., Hakomori S., Titani K.;
RT "Ribonuclease activity of sialic acid-binding lectin from Rana
RT catesbeiana eggs.";
RL Glycobiology 3:37-45(1993).
RN [5]
RP STRUCTURE BY NMR OF 23-133.
RX MEDLINE=98437383; PubMed=9761686;
RA Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;
RT "The solution structure of a cytotoxic ribonuclease from the oocytes
RT of Rana catesbeiana (bullfrog).";
RL J. Mol. Biol. 283:231-244(1998).
CC -!- FUNCTION: Preferentially cleaves single-stranded RNA at pyrimidine

```
Qy          34 CKRVNTFIISSATTVKAICTG----VINMNVLSTTRFQLNTCTRTSITPR-PCPYSSRTE 88
               || |||||  :   :||||        |    | : ||: ||     : | || | :
Db          39 CKEVNTFIHGTRNDIKAICNDKNGEPYNNFRRSKSPFQITTCKHKGGSNRPPCGYRATAG 98

Qy          89 TNYICVKCENQYPVHF 104
                 | | |||  ||||
Db          99 FRTIAVACENGLPVHF 114
```

RESULT 15
NRGPB
pancreatic ribonuclease (EC 3.1.27.5) B - guinea pig (tentative sequence)
N;Alternate names: RNase IB
C;Species: Cavia porcellus (guinea pig)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C;Accession: A00826
R;van den Berg, A.; van den Hende-Timmer, L.; Hofsteenge, J.; Gaastra, W.; Beintema, J.J
Eur. J. Biochem. 75, 91-100, 1977
A;Title: Guinea pig pancreatic ribonucleases. Isolation, properties, primary structure a
A;Reference number: A91247; MUID:77185023; PMID:862624
A;Accession: A00826
A;Molecule type: protein
A;Residues: 1-128 <VAN>
A;Note: 64-Pro was also found
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;21,34/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted

Query Match 19.5%; Score 118.5; DB 1; Length 128;
Best Local Similarity 31.6%; Pred. No. 8.5e-05;
Matches 37; Conservative 14; Mismatches 43; Indels 23; Gaps 6;

```
Qy           7 FQQKHI------INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60
               ||::|:       |:   || :|     :  |:|| ||||:  |   |:|:|      ||
Db           8 FQRQHMDPEGSPSNSSNYCNVMMIRR-NMTQGRCKPVNTFVHESLADVQAVC---FQKNV 63

Qy          61 L----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCENQ--YPVHF 104
               \          | :| ::  |  || :  | | |         | | ||     ||||
Db          64 LCKNGQTNCYQSYSRMRITDCRVTSSSKFPNCSYRMSQAQKSIIVACEGDPYVPVHF 120
```

Search completed: May 7, 2004, 21:54:55
Job time : 10.072 secs

```
Db          6 AKFERQHIDSNPSSVSSSNYCNQMMKSR-NLTQGRCKPVNTFVHESLADVQAVCS---QK 61

Qy         59 NVL----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 104

Db         62 NVACKNGQTNCYQSYSTMSITDCRETGSSKYPNCAYKTTQAKKHIIVACEGNPYVPVHY 120
```

RESULT 11
NRKGR
pancreatic ribonuclease (EC 3.1.27.5) - red kangaroo
N;Alternate names: RNase 1; RNase A
C;Species: Macropus rufus, Megaleia rufa (red kangaroo)
C;Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 04-Oct-1996
C;Accession: A00833
R;Gaastra, W.; Welling, G.W.; Beintema, J.J.
Eur. J. Biochem. 86, 209-217, 1978
A;Title: The amino-acid sequence of kangaroo pancreatic ribonuclease.
A;Reference number: A00833; MUID:78190621; PMID:658039
A;Accession: A00833
A;Molecule type: protein
A;Residues: 1-122 <GAA>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;11,40,117/Active site: His, Lys, His #status predicted
F;25-83,39-94,57-109,64-71/Disulfide bonds: #status predicted
F;61/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 20.1%; Score 122; DB 1; Length 122;
Best Local Similarity 30.7%; Pred. No. 3.6e-05;
Matches 35; Conservative 16; Mismatches 45; Indels 18; Gaps 6;

```
Qy          7 FQQKHI------INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAIC-------- 52

Db          7 FQRQHMDTEHSTASSSNYCNLMMKAR-DMTSGRCKPLNTFIHEPKSVVDAVCHQENVTCK 65

Qy         53 TGVINMNVLSTTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCENQY-PVHF 104

Db         66 NGRTNC-YKSNSRLSITNCRQTGASKYPNCQYETSNLNKQIIVACEGQYVPVHF 118
```

RESULT 12
NRCU
pancreatic ribonuclease (EC 3.1.27.5) - nutria (tentative sequence)
N;Alternate names: RNase 1; RNase A
C;Species: Myocastor coypus (nutria, coypu)
C;Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
C;Accession: A00822
R;van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
Biochim. Biophys. Acta 453, 400-409, 1976
A;Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic
A;Reference number: A90612; MUID:77065676; PMID:999896
A;Accession: A00822
A;Molecule type: protein
A;Residues: 1-128 <VAN>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F;34/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 19.9%; Score 120.5; DB 1; Length 128;
Best Local Similarity 31.6%; Pred. No. 5.4e-05;
Matches 37; Conservative 15; Mismatches 42; Indels 23; Gaps 7;

```
Qy          7 FQQKHI------INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60

Db          8 FERQHMDSRGSPSTNPNYCNEMMKSR-NMTQGRCKPVNTFVHEPLADVQAVC---FQKNV 63

Qy         61 L----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 104

Db         64 LCKNGQTNCYQSNSNMHITDCRVTSNSDYPNCSYRTSQEEKSIVVACEGNPYVPVHF 120
```

RESULT 13
NRMS
pancreatic ribonuclease (EC 3.1.27.5) precursor - mouse
N;Alternate names: RNase 1; RNase A
C;Species: Mus musculus (house mouse)
C;Date: 30-Nov-1980 #sequence_revision 13-Mar-1997 #text_change 18-Jun-1999
C;Accession: A34090; S22598; A00830
R;Schueller, C.; Nijssen, H.M.J.; Kok, R.; Beintema, J.J.
Mol. Biol. Evol. 7, 29-44, 1990
A;Title: Evolution of nucleic acids coding for ribonucleases: the mRNA sequence of mouse
A;Reference number: A34090; MUID:90136034; PMID:2299980
A;Accession: A34090
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-149 <SCH>
A;Cross-references: GB:M27814; NID:g200762; PIDN:AAA40060.1; PID:g200763
R;Samuelson, L.C.; Wiebauer, K.; Howard, G.; Schmid, R.M.; Koeplin, D.; Meisler, M.H.
Nucleic Acids Res. 19, 6935-6941, 1991
A;Title: Isolation of the murine ribonuclease gene Rib-1: structure and tissue specific e
A;Reference number: S22598; MUID:92107684; PMID:1840677
A;Accession: S22598
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-149 <SAM>
A;Cross-references: EMBL:X60103; NID:g53981; PIDN:CAA42697.1; PID:g53982
R;Lenstra, J.A.; Beintema, J.J.
Eur. J. Biochem. 98, 399-408, 1979
A;Title: The amino acid sequence of mouse pancreatic ribonuclease.
A;Reference number: A00830; MUID:80024269; PMID:556267
A;Accession: A00830
A;Molecule type: protein
A;Residues: 26-149 <LEN>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-149/Product: pancreatic ribonuclease #status experimental <MAT>
F;37,66,144/Active site: His, Lys, His #status predicted
F;51-109,65-120,83-135,90-97/Disulfide bonds: #status predicted
F;62,87/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.9%; Score 120.5; DB 1; Length 149;
Best Local Similarity 30.8%; Pred. No. 6.3e-05;
Matches 36; Conservative 16; Mismatches 42; Indels 23; Gaps 7;

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Qy          7 FQQKHI------INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60

Db         33 FQRQHMDPDGSSINSPTYCNQMMKRR-DMTNGSCKPVNTFVHEPLADVQAVCS---QENV 88

Qy         61 L----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 104

Db         89 TCKNRKSNCYKSSSALHITDCHLKGNSKYPNCDYKTTQYQKHIIVACEGNPYVPVHF 145
```

RESULT 14
A43825
angiogenin - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S29834; A43825
R;Bond, M.D.; Strydom, D.J.; Vallee, B.L.
Biochim. Biophys. Acta 1162, 177-186, 1993
A;Title: Characterization and sequencing of rabbit, pig and mouse angiogenins: discernmer
A;Reference number: S29833; MUID:93192291; PMID:8448182
A;Accession: S29834
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-123 <BON>
A;Note: this sequence was submitted to the Protein Sequence Database, December 1992
C;Superfamily: pancreatic ribonuclease

Query Match 19.7%; Score 119.5; DB 1; Length 123;
Best Local Similarity 39.5%; Pred. No. 6.5e-05;
Matches 30; Conservative 6; Mismatches 35; Indels 5; Gaps 2;

```
S20066
pancreatic-type ribonuclease (EC 3.1.27.5) BRb precursor, brain - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 22-Nov-1993 #sequence_revision 12-May-1995 #text_change 22-Jun-1999
C;Accession: S20066; JX0056
R;Sasso, M.P.; Carsana, A.; Confalone, E.; Cosi, C.; Sorrentino, S.; Viola, M.; Palmieri
Nucleic Acids Res. 19, 6469-6474, 1991
A;Title: Molecular cloning of the gene encoding the bovine brain ribonuclease and its ex
A;Reference number: S20066; MUID:92093604; PMID:1754384
A;Accession: S20066
A;Molecule type: DNA
A;Residues: 1-167 <SAS>
A;Cross-references: EMBL:X59767; NID:g150; PIDN:CAA42439.1; PID:g151
R;Watanabe, H.; Katoh, H.; Ishii, M.; Komoda, Y.; Sanda, A.; Takizawa, Y.; Ohgi, K.; Iri
J. Biochem. 104, 939-945, 1988
A;Title: Primary structure of a ribonuclease from bovine brain.
A;Reference number: JX0056; MUID:89214015; PMID:3243767
A;Accession: JX0056
A;Molecule type: protein
A;Residues: 27-154,'S',156-166 <WAT>
A;Experimental source: brain
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase
F;38,67,145/Active site: His, Lys, His #status predicted
F;52-110,66-121,84-136,91-98/Disulfide bonds: #status predicted
F;88/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;155/Binding site: carbohydrate (Thr) (covalent) #status experimental
F;159/Binding site: carbohydrate (Ser) (covalent) #status experimental

  Query Match             22.0%;  Score 133.5;  DB 2;  Length 167;
  Best Local Similarity   31.4%;  Pred. No. 3.6e-06;
  Matches   38;  Conservative   17;  Mismatches   43;  Indels   23;  Gaps    7;

Qy          5 ATFQQKHI------INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINM 58
              | |:::|:       :  |  || :|      :  |:|| |||| :  |   |||:|:
Db         32 AKFRRQHMDSGSSSSSNPNYCNQMMKRR-RMTHGRCKPVNTFVHESLDDVKAVCS---QK 87

Qy         59 NVL----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHFA 105
              |:          |  :   :  |  |  :  | | | :  :  || | || | | ||||
Db         88 NITCKNGHPNCYQSKSTMSITDCRETGSSKYPNCAYKTSQKQKYITVACEGNPYVPVHFD 147

Qy        106 G 106
              |
Db        148 G 148


RESULT 8
NRPG
pancreatic ribonuclease (EC 3.1.27.5) - pig
N;Alternate names: RNase 1; RNase A
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
C;Accession: A92071; A91391; A00816
R;Jackson, R.L.; Hirs, C.H.W.
J. Biol. Chem. 245, 637-653, 1970
A;Title: The primary structure of porcine pancreatic ribonuclease. II. The amino acid se
A;Reference number: A92071; MUID:70104197; PMID:5460946
A;Accession: A92071
A;Molecule type: protein
A;Residues: 1,'Q',3-124 <JAC>
R;Wierenga, R.K.; Huizinga, J.D.; Gaastra, W.; Welling, G.W.; Beintema, J.J.
FEBS Lett. 31, 181-185, 1973
A;Title: Affinity chromatography of porcine pancreatic ribonuclease and reinvestigation
A;Reference number: A91391
A;Accession: A91391
A;Molecule type: protein
A;Residues: 1-124 <WIE>
R;Phelan, J.J.; Hirs, C.H.W.
J. Biol. Chem. 245, 654-661, 1970
A;Title: The primary structure of porcine pancreatic ribonuclease. III. The disulfide bo
A;Reference number: A92072; MUID:70104198; PMID:4904878
A;Contents: annotation; disulfide bonds
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;21,34,76/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status experimental

  Query Match             21.8%;  Score 132.5;  DB 1;  Length 124;
  Best Local Similarity   31.6%;  Pred. No. 3.3e-06;
  Matches   36;  Conservative   19;  Mismatches   42;  Indels   17;  Gaps    6;

Qy          7 FQQKHI------INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGV-INMN 59
              ||::|:       |:   || :|      :  |:|| |||| :  |   |:|:|: : :|
Db          8 FQRQHMDPDSSSSNSSNYCNLMMSRR-NMTQGRCKPVNTFVHESLADVQAVCSQINVNCK 66

Qy         60 VLSTTRFQLNT------CTRTSITPRP-CPYSSRTETNYICVKCENQ--YPVHF 104
              |  :| |:       | :|  :  | | | :  |  :| | ||     ||||
Db         67 NGQTNCYQSNSTMHITDCRQTGSSKYPNCAYKASQEQKHIIVACEGNPPVPVHF 120


RESULT 9
S41111
pancreatic ribonuclease - common iguana
C;Species: Iguana iguana (common iguana)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Aug-1998
C;Accession: S41111
R;Zhao, W.; Beintema, J.J.; Hofsteenge, J.
Eur. J. Biochem. 219, 641-646, 1994
A;Title: The amino acid sequence of iguana (Iguana iguana) pancreatic ribonuclease.
A;Reference number: S41111; MUID:94139745; PMID:8307028
A;Accession: S41111
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-119 <ZHA>
C;Superfamily: pancreatic ribonuclease

  Query Match             21.7%;  Score 131.5;  DB 2;  Length 119;
  Best Local Similarity   30.4%;  Pred. No. 4e-06;
  Matches   35;  Conservative   16;  Mismatches   51;  Indels   13;  Gaps    4;

Qy          2 QNWATFQQKHI-------INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAIC-- 52
              |:|::|| |||        |   |: :|     :   :||  |||: :| : :: :|
Db          1 QDWSSFQNKHIDYPETSASNPNAYCDLMMQRR-NLNPTKCKTRNTFVHASPSEIQQVCGS 59

Qy         53 --TGVINMNVLSTTRFQLNTCTRTSIT-PRPCPYSSRTETNYICVKCENQYPVHF 104
               |   :  |  | |  |     | |  | |:    |  | : |||  ||||
Db         60 GGTHYEDNLYDSNESFDLTDCKNVGGTAPSSCKYNGTPGTKRIRIACENNQPVHF 114


RESULT 10
NRPRH
pancreatic ribonuclease (EC 3.1.27.5) - pronghorn (tentative sequence)
N;Alternate names: RNase 1; RNase A
C;Species: Antilocapra americana (pronghorn)
C;Date: 28-Feb-1981 #sequence_revision 28-Feb-1981 #text_change 31-Mar-2000
C;Accession: A00813
R;Beintema, J.J.; Gaastra, W.; Munniksma, J.
J. Mol. Evol. 13, 305-316, 1979
A;Title: Primary structure of pronghorn pancreatic ribonuclease: close relationship betw
A;Reference number: A00813; MUID:80075014; PMID:513141
A;Accession: A00813
A;Molecule type: protein
A;Residues: 1-124 <BEI>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F;34/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

  Query Match             20.2%;  Score 122.5;  DB 1;  Length 124;
  Best Local Similarity   30.3%;  Pred. No. 3.3e-05;
  Matches   36;  Conservative   18;  Mismatches   42;  Indels   23;  Gaps    7;

Qy          5 ATFQQKHIINTPI------ICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINM 58
              | |:::|| : |        || :| :   :  |:|| |||| :  |   |:|:|:
```

```
Qy          2 QNWATFQQKHIINTP-IICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGV-INMN 59
              |||| ||:||| ||  | |||||| :|||||||||  ||||||||||||||:|   | |
Db          1 QNWAKFQEKHIPNTSNINCNTIMDKSIYIVGGQCKERNTFIISSATTVKAICSGASTNRN 60

Qy         60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              |||||||||||| |::  ||||||:|||||| |||||||: ||||||||||
Db         61 VLSTTRFQLNTCIRSATAPRPCPYNSRTETNVICVKCENRLPVHFAGIGRC 111


RESULT 3
JX0085
pancreatic ribonuclease (EC 3.1.27.5) - bullfrog
C;Species: Rana catesbeiana (bullfrog)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994
C;Accession: JX0085
R;Nitta, R.; Katayama, N.; Okabe, Y.; Iwama, M.; Watanabe, H.; Abe, Y.; Okazaki, T.; Ohg
J. Biochem. 106, 729-735, 1989
A;Title: Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver.
A;Reference number: JX0085; MUID:90130374; PMID:2613682
A;Accession: JX0085
A;Molecule type: protein
A;Residues: 1-111 <NIT>
C;Superfamily: pancreatic ribonuclease
C;Keywords: hydrolase; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10,35,104/Active site: His, Lys, His #status predicted
F;19-72,34-82,52-97,94-111/Disulfide bonds: #status predicted

  Query Match             61.6%;  Score 374;  DB 2;  Length 111;
  Best Local Similarity   65.8%;  Pred. No. 2.8e-30;
  Matches   73;  Conservative    9;  Mismatches   27;  Indels    2;  Gaps    2;

Qy          2 QNWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 59
              |||| |::||| :|  | ||||||  ||||||:||  |||||||   |||||:||  :
Db          1 QNWAKFKEKHIRSTSSIDCNTIMDKAIYIVGGKCKERNTFIISSEDNVKAICSGVSPDRK 60

Qy         60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              |||| |:|||| | |||||||||     : | |||||| | |||| |||:|
Db         61 ELSTTSFKLNTCIRDSITPRPCPYHPSPDNNKICVKCEKQLPVHFVGIGKC 111


RESULT 4
A39035
ribonuclease-related anti-tumor protein - northern leopard frog (fragment)
C;Species: Rana pipiens (northern leopard frog)
C;Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993
C;Accession: A39035
R;Ardelt, W.; Mikulski, S.M.; Shogen, K.
J. Biol. Chem. 266, 245-251, 1991
A;Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and earl
A;Reference number: A39035; MUID:91093131; PMID:1985896
A;Accession: A39035
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-104 <ARD>
C;Superfamily: pancreatic ribonuclease

  Query Match             45.2%;  Score 274.5;  DB 2;  Length 104;
  Best Local Similarity   48.6%;  Pred. No. 2.1e-20;
  Matches   54;  Conservative   16;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          2 QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 59
              ::| |||:||| ||  : |: ||  |::     ||  |||| |    ||||| |:| : |
Db          1 EDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56

Qy         60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              ||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104


RESULT 5
NRWHK
pancreatic ribonuclease (EC 3.1.27.5) - minke whale
N;Alternate names: RNase 1; RNase A
C;Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
C;Accession: A00818
R;Emmens, M.; Welling, G.W.; Beintema, J.J.
Biochem. J. 157, 317-323, 1976
A;Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclease.
A;Reference number: A00818; MUID:76277855; PMID:962870
A;Accession: A00818
A;Molecule type: protein
A;Residues: 1-124 <EMM>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F;76/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

  Query Match             22.3%;  Score 135.5;  DB 1;  Length 124;
  Best Local Similarity   33.3%;  Pred. No. 1.7e-06;
  Matches   39;  Conservative   16;  Mismatches   39;  Indels   23;  Gaps    7;

Qy          7 FQQKHII------NTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60
              ||::|:       | |  || :|     :  |:|| ||||:  |   |||:|:     ||
Db          8 FQRQHMDSGNSPGNNPNYCNQMMMRR-KMTQGRCKPVNTFVHESLEDVKAVCS---QKNV 63

Qy         61 L----------STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 104
              |          | :   :  | :|  :  | | | :  :  :| | || | | ||||
Db         64 LCKNGRTNCYESNSTMHITDCRQTGSSKYPNCAYKTSQKEKHIIVACEGNPYVPVHF 120


RESULT 6
A35932
angiogenin precursor - mouse
N;Alternate names: angiogenesis factor
N;Contains: ribonuclease (EC 3.1.27.-)
C;Species: Mus musculus (house mouse)
C;Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 18-Jun-1999
C;Accession: A35932
R;Bond, M.D.; Vallee, B.L.
Biochem. Biophys. Res. Commun. 171, 988-995, 1990
A;Title: Isolation and sequencing of mouse angiogenin DNA.
A;Reference number: A35932; MUID:91025023; PMID:2222458
A;Accession: A35932
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-145 <BON>
A;Cross-references: GB:U22516; NID:g726325; PIDN:AAA91366.1; PID:g726326
C;Genetics:
A;Introns: #status absent
C;Function:
A;Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues
C;Superfamily: pancreatic ribonuclease
C;Keywords: angiogenesis; hydrolase; nucleic acid degradation; pyroglutamic acid
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-145/Product: angiogenin #status predicted <MAT>
F;25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;37,64,137/Active site: His, Lys, His #status predicted
F;50-104,63-115,81-130/Disulfide bonds: #status predicted

  Query Match             22.3%;  Score 135.5;  DB 1;  Length 145;
  Best Local Similarity   39.5%;  Pred. No. 2e-06;
  Matches   30;  Conservative   12;  Mismatches   29;  Indels    5;  Gaps    3;

Qy         34 CKRVNTFIISSATTVKAIC---TGVINMNV-LSTTRFQLNTCTRTSITPR-PCPYSSRTE 88
              || |||||  : : :||||          |: :| : ||: ||  |  :|| || | :
Db         63 CKDVNTFIHGNKSNIKAICGANGSPYRENLRMSKSPFQVTTCKHTGGSPRPPCQYRASAG 122

Qy         89 TNYICVKCENQYPVHF 104
                :: : |||  ||||
Db        123 FRHVVIACENGLPVHF 138


RESULT 7
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 7, 2004, 21:38:36 ; Search time 10.072 Seconds
(without alignments)
1060.090 Million cell updates/sec

Title: US-09-961-400-17
Perfect score: 607
Sequence: 1 MQNWATFQQKHIINTPIICN.....ICVKCENQYPVHFAGIGRCP 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	588.5	97.0	111	2	A27121	ribonuclease-relat
2	455	75.0	111	1	JX0120	ribonuclease-relat
3	374	61.6	111	2	JX0085	pancreatic ribonuc
4	274.5	45.2	104	2	A39035	ribonuclease-relat
5	135.5	22.3	124	1	NRWHK	pancreatic ribonuc
6	135.5	22.3	145	1	A35932	angiogenin precurs
7	133.5	22.0	167	2	S20066	pancreatic-type ri
8	132.5	21.8	124	1	NRPG	pancreatic ribonuc
9	131.5	21.7	119	2	S41111	pancreatic ribonuc
10	122.5	20.2	124	1	NRPRH	pancreatic ribonuc
11	122	20.1	122	1	NRKGR	pancreatic ribonuc
12	120.5	19.9	128	1	NRCU	pancreatic ribonuc
13	120.5	19.9	149	1	NRMS	pancreatic ribonuc
14	119.5	19.7	123	1	A43825	angiogenin - pig
15	118.5	19.5	128	1	NRGPB	pancreatic ribonuc
16	117.5	19.4	128	1	NRHO	pancreatic ribonuc
17	116.5	19.2	124	1	NRCM	pancreatic ribonuc
18	116.5	19.2	124	1	NRCMM	pancreatic ribonuc
19	116.5	19.2	124	1	NRCMB	pancreatic ribonuc
20	116.5	19.2	128	1	NRKS	pancreatic ribonuc
21	114.5	18.9	124	2	S08549	ribonuclease - dom
22	114	18.8	125	1	A32474	angiogenin [valida
23	113.5	18.7	124	1	NRDEN	pancreatic ribonuc
24	113	18.6	147	1	NRHUAG	angiogenin precurs
25	112.5	18.5	124	1	NRGF	pancreatic ribonuc
26	112.5	18.5	124	1	NRDEO	pancreatic ribonuc
27	112	18.5	125	1	B43825	angiogenin - rabbi
28	111.5	18.4	130	2	S22808	pancreatic ribonuc
29	110.5	18.2	124	1	NRBOB	pancreatic ribonuc
30	110.5	18.2	124	1	NRWB	pancreatic ribonuc
31	110.5	18.2	124	1	NREKN	pancreatic ribonuc
32	110.5	18.2	124	2	S07141	pancreatic ribonuc
33	110.5	18.2	150	1	NRBO	pancreatic ribonuc
34	110.5	18.2	158	2	I61900	eosinophil-derived
35	109.5	18.0	124	1	NRSH	pancreatic ribonuc
36	108.5	17.9	119	2	JX0115	pancreatic ribonuc
37	108.5	17.9	124	1	NRCB	pancreatic ribonuc
38	108.5	17.9	152	1	NRRT	pancreatic ribonuc
39	106.5	17.5	124	1	NRHP	pancreatic ribonuc
40	106.5	17.5	125	4	A47498	seminal ribonuclea
41	106.5	17.5	150	1	NRBOS	seminal ribonuclea
42	104.5	17.2	124	1	NRGN	pancreatic ribonuc
43	104.5	17.2	124	1	NRDEF	pancreatic ribonuc
44	104	17.1	125	2	S04503	pancreatic ribonuc
45	103.5	17.1	124	2	S08546	pancreatic ribonuc

ALIGNMENTS

RESULT 1
A27121
ribonuclease-related sialic acid-binding lectin - bullfrog
C;Species: Rana catesbeiana (bullfrog)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 30-Jun-1993
C;Accession: A27121
R;Titani, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kawauchi, H.; Takayanag
Biochemistry 26, 2189-2194, 1987
A;Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana)
A;Reference number: A27121; MUID:87299649; PMID:3304421
A;Accession: A27121
A;Molecule type: protein
A;Residues: 1-111 <TIT>
C;Superfamily: pancreatic ribonuclease
C;Keywords: lectin

Query Match 97.0%; Score 588.5; DB 2; Length 111;
Best Local Similarity 98.2%; Pred. No. 1.3e-51;
Matches 109; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

```
Qy          2 QNWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60
              :|||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db          1 ENWATFQQKHIINTPIINCNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60

Qy         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
```

RESULT 2
JX0120
ribonuclease-related sialic acid-binding lectin - Japanese frog
C;Species: Rana japonica (Japanese frog)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JX0120
R;Kamiya, Y.; Oyama, F.; Oyama, R.; Sakakibara, F.; Nitta, K.; Kawauchi, H.; Takayanagi,
J. Biochem. 108, 139-143, 1990
A;Title: Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs.
A;Reference number: JX0120; MUID:91035319; PMID:2229005
A;Accession: JX0120
A;Molecule type: protein
A;Residues: 1-111 <KAM>
A;Experimental source: egg
C;Superfamily: pancreatic ribonuclease
C;Keywords: lectin; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;19-72,34-82,52-97,94-111/Disulfide bonds: #status experimental

Query Match 75.0%; Score 455; DB 1; Length 111;
Best Local Similarity 78.4%; Pred. No. 2.5e-38;
Matches 87; Conservative 7; Mismatches 15; Indels 2; Gaps 2;

```
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens
;   OTHER INFORMATION: ribonuclease with Met at position 1 (recombinant
;   OTHER INFORMATION: Met(-1) RaPLR1)
US-09-948-391A-6

  Query Match             47.2%;  Score 286.5;  DB 10;  Length 105;
  Best Local Similarity   50.0%;  Pred. No. 7.5e-25;
  Matches   56;  Conservative   15;  Mismatches   32;  Indels    9;  Gaps    4;

Qy          1 MQNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NM 58
              ||:| |||:||: ||  : || ||  |::    ||  |||| |    ||||| |:| :
Db          1 MQDWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASK 56

Qy         59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
              |||:|: | |: |   ::| ||| |  :  ||  || |||| |||| |:| |
Db         57 NVLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105


Search completed: May  7, 2004, 21:51:58
Job time : 36.6155 secs
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; GENERAL INFORMATION:
;  APPLICANT: RYBAK, SUSANNA M.
;  APPLICANT:  GOLDENBERG, DAVID M.
;  APPLICANT:  NEWTON, DIANNE L.
;  TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
;  TITLE OF INVENTION:  CELLS
;  FILE REFERENCE: 018733/1059
;  CURRENT APPLICATION NUMBER: US/09/961,400
;  CURRENT FILING DATE:  2001-09-25
;  PRIOR APPLICATION NUMBER: 09/622,613
;  PRIOR FILING DATE: 2000-08-17
;  PRIOR APPLICATION NUMBER: PCT/US99/06641
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: 60/079,751
;  PRIOR FILING DATE: 1998-03-26
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: Rana catesbeiana
US-09-961-400-24

  Query Match             98.4%;  Score 597;  DB 10;  Length 110;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-60;
  Matches  109;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 NWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS 62
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Db          2 NWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS 61

Qy         63 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
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Db         62 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110


RESULT 13
US-09-961-400-19
; Sequence 19, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
;  APPLICANT: RYBAK, SUSANNA M.
;  APPLICANT:  GOLDENBERG, DAVID M.
;  APPLICANT:  NEWTON, DIANNE L.
;  TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
;  TITLE OF INVENTION:  CELLS
;  FILE REFERENCE: 018733/1059
;  CURRENT APPLICATION NUMBER: US/09/961,400
;  CURRENT FILING DATE:  2001-09-25
;  PRIOR APPLICATION NUMBER: 09/622,613
;  PRIOR FILING DATE: 2000-08-17
;  PRIOR APPLICATION NUMBER: PCT/US99/06641
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: 60/079,751
;  PRIOR FILING DATE: 1998-03-26
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: Rana catesbeiana
US-09-961-400-19

  Query Match             98.2%;  Score 596;  DB 10;  Length 110;
  Best Local Similarity   98.2%;  Pred. No. 4e-60;
  Matches  108;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 QNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 61
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Db          1 QNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 60

Qy         62 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110


RESULT 14
US-09-948-391A-19
; Sequence 19, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
;  APPLICANT: Rybak, Susanna M.
;  APPLICANT:  Newton, Dianne L.
;  APPLICANT:  The United States of America
;  APPLICANT:  as represented by The Secretary of the
;  APPLICANT:  Department of Health and Human Services
;  TITLE OF INVENTION: Recombinant Anti-Tumor RNase
;  FILE REFERENCE: 015280-343110US
;  CURRENT APPLICATION NUMBER: US/09/948,391A
;  CURRENT FILING DATE:  2002-05-10
;  PRIOR APPLICATION NUMBER: US 60/079,751
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: WO PCT/US99/06641
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: US 09/622,613
;  PRIOR FILING DATE: 2000-08-17
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Rana
;   OTHER INFORMATION: catesbeiana ribonuclease with Met22Leu and
;   OTHER INFORMATION: Met57Leu substitutions (recombinant RaCOR1
;   OTHER INFORMATION: Met22Leu Met57Leu)
US-09-948-391A-19

  Query Match             97.2%;  Score 590;  DB 10;  Length 110;
  Best Local Similarity   97.3%;  Pred. No. 2e-59;
  Matches  107;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 QNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 61
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Db          1 QNWATFQQKHIIKTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 60

Qy         62 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
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Db         61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110


RESULT 15
US-09-948-391A-6
; Sequence 6, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
;  APPLICANT: Rybak, Susanna M.
;  APPLICANT:  Newton, Dianne L.
;  APPLICANT:  The United States of America
;  APPLICANT:  as represented by The Secretary of the
;  APPLICANT:  Department of Health and Human Services
;  TITLE OF INVENTION: Recombinant Anti-Tumor RNase
;  FILE REFERENCE: 015280-343110US
;  CURRENT APPLICATION NUMBER: US/09/948,391A
;  CURRENT FILING DATE:  2002-05-10
;  PRIOR APPLICATION NUMBER: US 60/079,751
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: WO PCT/US99/06641
;  PRIOR FILING DATE: 1999-03-26
;  PRIOR APPLICATION NUMBER: US 09/622,613
;  PRIOR FILING DATE: 2000-08-17
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 105
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